

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 17, 2005, 08:52:18 ; Search time 25 Seconds

(without alignments)
1397.430 Million cell updates/sec

Title: US-10-033-350-2

Perfect score: 2488

Sequence: 1 MFLLATYFPLPLDLMSAB.....PVLMFLALALSLVSLAETS 468

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2488	100.0	468	3	US-08-802-805D-21
2	2488	100.0	468	4	US-08-837-199A-4
3	2488	100.0	468	4	US-08-860-370-2
4	2488	100.0	468	4	US-09-187-906-2
5	2488	100.0	468	4	US-08-861-990-1
6	2488	100.0	468	4	US-09-388-316C-21
7	2316.5	93.1	465	4	US-08-837-199A-2
8	2316.5	93.1	465	4	US-09-388-316C-22
9	2311.5	92.9	463	4	US-08-837-199A-12
10	2310.5	92.9	465	4	US-08-861-990-8
11	2309.5	92.8	465	4	US-08-837-199A-6
12	2306.5	92.7	463	4	US-08-837-199A-10
13	2278	91.6	460	3	US-08-802-805D-22
14	2278	91.6	460	4	US-09-187-906-11
15	1686	67.8	346	4	US-09-187-906-9
16	1431.5	57.5	294	4	US-08-837-199A-16
17	1120.5	45.0	232	4	US-08-837-199A-14
18	1120.5	45.0	464	3	US-08-957-063-6
19	1120.5	45.0	464	3	US-09-487-685-6
20	1120.5	45.0	464	3	US-08-802-805D-6
21	1120.5	45.0	464	4	US-08-861-990-2
22	1120.5	45.0	464	4	US-09-388-316C-6
23	1117.5	44.9	464	3	US-08-957-063-3
24	1117.5	44.9	464	3	US-09-487-685-3
25	1117.5	44.9	464	3	US-08-802-805D-3
26	1117.5	44.9	464	4	US-09-388-316C-13
27	1109.5	44.6	464	4	US-09-187-906-13

28	1108.5	44.6	464	4	US-08-861-990-9	Sequence 9, Appl
29	1100	44.2	664	3	US-08-957-063-18	Sequence 18, Appl
30	1100	44.2	664	3	US-09-487-685-18	Sequence 18, Appl
31	1100	44.2	664	3	US-08-802-805D-18	Sequence 18, Appl
32	1100	44.2	664	4	US-09-388-316C-18	Sequence 18, Appl
33	1099.5	44.2	664	3	US-08-957-063-16	Sequence 16, Appl
34	1099.5	44.2	664	3	US-09-487-685-16	Sequence 16, Appl
35	1099.5	44.2	664	3	US-08-802-805D-16	Sequence 16, Appl
36	1099.5	44.2	664	4	US-09-388-316C-16	Sequence 16, Appl
37	1098.5	44.2	445	4	US-08-861-990-11	Sequence 11, Appl
38	1098.5	44.2	219	4	US-08-837-199A-18	Sequence 18, Appl
39	983.5	39.5	209	4	US-08-837-199A-20	Sequence 20, Appl
40	646.5	26.0	147	4	US-08-837-199A-22	Sequence 22, Appl
41	617.5	24.8	141	4	US-08-837-199A-24	Sequence 24, Appl
42	511	20.5	400	3	US-09-220-528-63	Sequence 63, Appl
43	511	20.5	400	3	US-09-187-906-21	Sequence 21, Appl
44	511	20.5	400	4	US-09-487-685-21	Sequence 21, Appl
45	505.5	20.3	397	3	US-09-220-528-64	Sequence 64, Appl

ALIGNMENTS

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RESULT 1
US-08-802-805D-21
Sequence 21, Application US/08802805D
Patent No. 6372453
APPLICANT: Robert D. Klein
TITLE OF INVENTION: Neuturin Receptor
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802, 805D
FILING DATE: 18-Feb-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Phd., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ. ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-802-805D-21
Query Match 100.0%; Score 2488; DB 3; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.1e-233; Indels 0; Gaps 0;
Matches 468; Conservative 0; Mismatches 0;
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QY 1 MFLLATYFPLPLDLMSABVSGDRLDVCKASDQCKXOSGCTKYRTLRQVAGKETNF 60
DB 1 MFLLATYFPLPLDLMSABVSGDRLDVCKASDQCKXOSGCTKYRTLRQVAGKETNF 60
QY 61 SLTSGLEADDEGRSAMEALKOKSLVNCRCRKGKKEKNCRLRIYMSYQSLQGNLLEDSF 120
DB 61 SLTSGLEADDEGRSAMEALKOKSLVNCRCRKGKKEKNCRLRIYMSYQSLQGNLLEDSF 120

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QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDDTCKKYSAYITPCTT 180
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QY 181 SMSNEVCNRRCKHAKLROFPDKVPKSHSYGMLFCSCRDIACTERRRQTTVPVCSYEERBR 240
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DB 241 PNCISLSDSCKTNYICRSRLADFTNCPESHRSVNCLENKADCLLAYSGLIGVMTNPN 300
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DB 301 YVDSSSLVAPWCDSCNSGNDLEDCLKFLNFKONTCLKNAIQAFNGSDVTMMQAPAPV 360
QY 361 QTTTATTTTARVKNKPLGPAAGSENEIPTHVLPCCANLQAQKLKSNVSGSTHLCLSDSDF 420
DB 361 QTTTATTTTARVKNKPLGPAAGSENEIPTHVLPCCANLQAQKLKSNVSGSTHLCLSDSDF 420
QY 421 GKDGLAGASHITTKSMAPPCSLSLPVMLTALAALLSVSLAETS 468
DB 421 GKDGLAGASHITTKSMAPPCSLSLPVMLTALAALLSVSLAETS 468

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RESULT 2 US-08-837-199A-4

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; Sequence 4, Application US/08837199A
; Patent No. 6453277
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUQIAN
; APPLICANT: MEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/08/837.199A
; CURRENT FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; LENGTH: 468
; TYPE: PRT
; ORGANISM: RAT
US-08-837-199A-4

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Query Match 100.0%; Score 2488; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 5,1e-233;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MFATLYPALDLILMSAEVSGGDRLDVCVASDCLKEQSGSTYRTLRQCVAKETNF 60
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DB 61 SLTSGLEAKDECRAMEALKQKSLVNCRCRGMKEKXCLRTYMSWOSLOQNDLLEDSF 120
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DB 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDDTCKKYSAYITPCTT 180
QY 181 SMSNEVCNRRCKHAKLROFPDKVPKSHSYGMLFCSCRDIACTERRRQTTVPVCSYEERBR 240
DB 181 SMSNEVCNRRCKHAKLROFPDKVPKSHSYGMLFCSCRDIACTERRRQTTVPVCSYEERBR 240
QY 241 PNCISLSDSCKTNYICRSRLADFTNCPESHRSVNCLENKADCLLAYSGLIGVMTNPN 300
DB 241 PNCISLSDSCKTNYICRSRLADFTNCPESHRSVNCLENKADCLLAYSGLIGVMTNPN 300

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QY 301 YVDSSSLVAPWCDSCNSGNDLEDCLKFLNFKONTCLKNAIQAFNGSDVTMMQAPAPV 360
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QY 361 QTTTATTTTARVKNKPLGPAAGSENEIPTHVLPCCANLQAQKLKSNVSGSTHLCLSDSDF 420
DB 361 QTTTATTTTARVKNKPLGPAAGSENEIPTHVLPCCANLQAQKLKSNVSGSTHLCLSDSDF 420
QY 421 GKDGLAGASHITTKSMAPPCSLSLPVMLTALAALLSVSLAETS 468
DB 421 GKDGLAGASHITTKSMAPPCSLSLPVMLTALAALLSVSLAETS 468

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RESULT 3 US-08-860-370-2

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; Sequence 2, Application US/08860370
; Patent No. 6504007
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Klein, Robert D.
; APPLICANT: Moore, Mark W.
; APPLICANT: Rosenthal, Arnon
; APPLICANT: Ryan, Anne M.
; TITLE OF INVENTION: USES OF GDNF AND GDNF RECEPTOR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

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COMPUTER READABLE FORM:

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MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/04363
FILING DATE: 13-Mar-1997
APPLICATION NUMBER: 08/615902
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/618236
FILING DATE: 14-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P0996P1PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-9874
TELEFAX: 650/225-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
FEATURES:
NAME/KEY: Extracellular Domain
LOCATION: 25
OTHER INFORMATION:
FEATURE:
NAME/KEY: Mature Protein N-terminal
LOCATION: 25-427
IDENTIFICATION METHOD:
OTHER INFORMATION:
FEATURE:
NAME/KEY: Potential Glycosylation Site

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LOCATION: 349
IDENTIFICATION METHOD:
OTHER INFORMATION:
FEATURE:
NAME/KEY: Potential Glycosylation Site
LOCATION: 408
IDENTIFICATION METHOD:
OTHER INFORMATION:
FEATURE:
NAME/KEY: Potential Glycosylation Site
LOCATION: 61
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-860-370-2

Query Match 100.0%; Score 2488; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.1e-233;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFATLYFALPLDLMSAEVSGGDRDLCYKASDOCLKEOSCTKRTTLQCVAGKETNF 60
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DB 121 YEFVNSRLSDIFRAVPEISDVFOQVEHISKGNCLDAKACNLDTCCKYRSAYITPCTT 180
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DB 181 SMNEVCNRRKCHALRQFPDKYPAKSYGMFLFCSCRDIACTERRRQTIYPVCSYERER 240
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DB 181 SMNEVCNRRKCHALRQFPDKYPAKSYGMFLFCSCRDIACTERRRQTIYPVCSYERER 240
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DB 301 YVDSSLSVAPWDCNSGNDLEDCLKFLNFFKONTCLKNAIQAFNGSDVTMMQAPAPV 360
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DB 361 QTTTATTTTAFRYKPKPLGAGSENEIPTHVLPCCANLQAKLSNVSGSTHCLSDSDP 420
QY 421 GKXGLAGASHITTKSMAPPSCLSLPVLMTALAAISVSLAETS 468
DB 421 GKXGLAGASHITTKSMAPPSCLSLPVLMTALAAISVSLAETS 468

RESULT 4
US-09-187-906-2
Sequence 2, Application US/09187906
Patent No. 6677135
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
TITLE OF INVENTION: and Renal Growth
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Biogen, Inc.
STREET: 14 Cambridge Center
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02142
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/187, 906
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/07726
FILING DATE: 07-MAY-97
APPLICATION NUMBER: US 60/017,427
FILING DATE: 08-MAY-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,300
FILING DATE: 07-JUN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/021,859
FILING DATE: 16-JUL-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/043,533
FILING DATE: 10-APR-97
ATTORNEY/AGENT INFORMATION:
NAME: Kaplan, Warren A.
REGISTRATION NUMBER: 34,199
REFERENCE/DOCKET NUMBER: A008 PCT CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-679-2400
TELEFAX: 617-679-2838
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-187-906-2

Query Match 100.0%; Score 2488; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.1e-233;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFATLYFALPLDLMSAEVSGGDRDLCYKASDOCLKEOSCTKRTTLQCVAGKETNF 60
DB 1 MFATLYFALPLDLMSAEVSGGDRDLCYKASDOCLKEOSCTKRTTLQCVAGKETNF 60
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DB 61 SLTSGLEAKDECSAMEALQKSLVNCRCRKGKKEKNCRIYWSMYQSLQGNLDLSDP 120
QY 121 YEFVNSRLSDIFRAVPEISDVFOQVEHISKGNCLDAKACNLDTCCKYRSAYITPCTT 180
DB 121 YEFVNSRLSDIFRAVPEISDVFOQVEHISKGNCLDAKACNLDTCCKYRSAYITPCTT 180
QY 121 YEFVNSRLSDIFRAVPEISDVFOQVEHISKGNCLDAKACNLDTCCKYRSAYITPCTT 180
DB 121 YEFVNSRLSDIFRAVPEISDVFOQVEHISKGNCLDAKACNLDTCCKYRSAYITPCTT 180
QY 181 SMNEVCNRRKCHALRQFPDKYPAKSYGMFLFCSCRDIACTERRRQTIYPVCSYERER 240
DB 181 SMNEVCNRRKCHALRQFPDKYPAKSYGMFLFCSCRDIACTERRRQTIYPVCSYERER 240
QY 181 SMNEVCNRRKCHALRQFPDKYPAKSYGMFLFCSCRDIACTERRRQTIYPVCSYERER 240
DB 181 SMNEVCNRRKCHALRQFPDKYPAKSYGMFLFCSCRDIACTERRRQTIYPVCSYERER 240
QY 241 PNCLSLDQSCNTYICRSRLADFFTNCOPEBSRSVSNCLKENYADCLAYSGLIGTWTPN 300
DB 241 PNCLSLDQSCNTYICRSRLADFFTNCOPEBSRSVSNCLKENYADCLAYSGLIGTWTPN 300
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DB 301 YVDSSLSVAPWDCNSGNDLEDCLKFLNFFKONTCLKNAIQAFNGSDVTMMQAPAPV 360
QY 361 QTTTATTTTAFRYKPKPLGAGSENEIPTHVLPCCANLQAKLSNVSGSTHCLSDSDP 420
DB 361 QTTTATTTTAFRYKPKPLGAGSENEIPTHVLPCCANLQAKLSNVSGSTHCLSDSDP 420
QY 421 GKXGLAGASHITTKSMAPPSCLSLPVLMTALAAISVSLAETS 468
DB 421 GKXGLAGASHITTKSMAPPSCLSLPVLMTALAAISVSLAETS 468

RESULT 5
US-08-861-990-1
Sequence 1, Application US/08861990
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Patent No. 6696259
GENERAL INFORMATION:
APPLICANT: Idenez, Carlos F.
APPLICANT: Arumae, Urmaz
APPLICANT: Sariola, Hannu
APPLICANT: Savanto, Petro
APPLICANT: Trupp, Miles
APPLICANT: Saarna, Mart
TITLE OF INVENTION: Glial Cell Line-Derived Neurotrophic Factor Receptors
FILE REFERENCE: CEPH0418
CURRENT APPLICATION NUMBER: US/08/861,990
PRIORITY FILING DATE: 1997-05-22
PRIORITY APPLICATION NUMBER: 08/747,842
PRIORITY FILING DATE: 1996-11-13
PRIORITY APPLICATION NUMBER: 60/006,619
PRIORITY FILING DATE: 1995-11-13
PRIORITY APPLICATION NUMBER: 60/015,767
PRIORITY FILING DATE: 1996-04-16
PRIORITY APPLICATION NUMBER: 60/021,965
PRIORITY FILING DATE: 1996-06-27
PRIORITY APPLICATION NUMBER: 60/020,638
PRIORITY FILING DATE: 1996-06-27
PRIORITY APPLICATION NUMBER: 60/020,639
PRIORITY FILING DATE: 1996-06-27
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 468
TYPE: PRT
ORGANISM: Rattus sp.
US-08-861-990-1
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Query Match          100.0%; Score 2488; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 5,1e-233;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFATLYPALPLDLMSAEVSGDRDLDCVKSADQCKECSCTKYRTLQCVAGKETNF 60
DB 1 MFATLYPALPLDLMSAEVSGDRDLDCVKSADQCKECSCTKYRTLQCVAGKETNF 60
QY 61 SLTSGLEAKDCRSAMEALKOKSLYNCRCKRMKKEKNCLRTIYMSYOSLGNDLLEDS 120
DB 61 SLTSGLEAKDCRSAMEALKOKSLYNCRCKRMKKEKNCLRTIYMSYOSLGNDLLEDS 120
QY 121 YEPNRSRSDI.FRAVPFISDVFOQVEHISKNNCLDAKACNLDDTCKKRSAYITPCTT 180
DB 121 YEPNRSRSDI.FRAVPFISDVFOQVEHISKNNCLDAKACNLDDTCKKRSAYITPCTT 180
QY 181 SMSNEVCNRKCHKALROFDFKVPKHSYGM.FCSCRDIACTERRRQTIIVPVCSEERER 240
DB 181 SMSNEVCNRKCHKALROFDFKVPKHSYGM.FCSCRDIACTERRRQTIIVPVCSEERER 240
QY 241 PNCISLQDSCKTNYICRSRLADPFTNCOPESSRSVSNCLKENYADCLAYSGLIGVTMPN 300
DB 241 PNCISLQDSCKTNYICRSRLADPFTNCOPESSRSVSNCLKENYADCLAYSGLIGVTMPN 300
QY 301 YVDSLSLVAAPWCDCSNGNDLEDCIKELNFKONTCLKNAIQAFNGSDVTMMQAPAPV 360
DB 301 YVDSLSLVAAPWCDCSNGNDLEDCIKELNFKONTCLKNAIQAFNGSDVTMMQAPAPV 360
QY 361 OTTATTTTAAFRVKNKPLGPAGSENEIPTHVLPNCANIQAOKLKSNSVSGSTHCLSDSD 420
DB 361 OTTATTTTAAFRVKNKPLGPAGSENEIPTHVLPNCANIQAOKLKSNSVSGSTHCLSDSD 420
QY 421 GKDGAGASSHTTTKSMAPPSCSLSL.PVLM.TALAAALSVSLAETS 468
DB 421 GKDGAGASSHTTTKSMAPPSCSLSL.PVLM.TALAAALSVSLAETS 468
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RESULT 6
US-09-388-316C-21
Sequence 21, Application US/09388316C
Patent No. 6777196
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```
GENERAL INFORMATION:
APPLICANT: KLEIN, ROBERT D.
APPLICANT: ROSENTHAL, ARNON
APPLICANT: HYNES, MARY A.
TITLE OF INVENTION: NEURTURIN RECEPTOR
FILE REFERENCE: GENENT.45A2DV1
CURRENT APPLICATION NUMBER: US/09/388,316C
CURRENT FILING DATE: 1999-09-01
PRIORITY APPLICATION NUMBER: 09/024,665
PRIORITY FILING DATE: 1998-02-17
PRIORITY APPLICATION NUMBER: 60/063,258
PRIORITY FILING DATE: 1997-10-24
PRIORITY APPLICATION NUMBER: 60/049,818
PRIORITY FILING DATE: 1997-06-09
PRIORITY APPLICATION NUMBER: 60/038,839
PRIORITY FILING DATE: 1997-02-18
SOFTWARE: FastSeq for Windows Version 4.0
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 21
LENGTH: 468
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-388-316C-21
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Query Match          100.0%; Score 2488; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 5,1e-233;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFATLYPALPLDLMSAEVSGDRDLDCVKSADQCKECSCTKYRTLQCVAGKETNF 60
DB 1 MFATLYPALPLDLMSAEVSGDRDLDCVKSADQCKECSCTKYRTLQCVAGKETNF 60
QY 61 SLTSGLEAKDCRSAMEALKOKSLYNCRCKRMKKEKNCLRTIYMSYOSLGNDLLEDS 120
DB 61 SLTSGLEAKDCRSAMEALKOKSLYNCRCKRMKKEKNCLRTIYMSYOSLGNDLLEDS 120
QY 121 YEPNRSRSDI.FRAVPFISDVFOQVEHISKNNCLDAKACNLDDTCKKRSAYITPCTT 180
DB 121 YEPNRSRSDI.FRAVPFISDVFOQVEHISKNNCLDAKACNLDDTCKKRSAYITPCTT 180
QY 181 SMSNEVCNRKCHKALROFDFKVPKHSYGM.FCSCRDIACTERRRQTIIVPVCSEERER 240
DB 181 SMSNEVCNRKCHKALROFDFKVPKHSYGM.FCSCRDIACTERRRQTIIVPVCSEERER 240
QY 241 PNCISLQDSCKTNYICRSRLADPFTNCOPESSRSVSNCLKENYADCLAYSGLIGVTMPN 300
DB 241 PNCISLQDSCKTNYICRSRLADPFTNCOPESSRSVSNCLKENYADCLAYSGLIGVTMPN 300
QY 301 YVDSLSLVAAPWCDCSNGNDLEDCIKELNFKONTCLKNAIQAFNGSDVTMMQAPAPV 360
DB 301 YVDSLSLVAAPWCDCSNGNDLEDCIKELNFKONTCLKNAIQAFNGSDVTMMQAPAPV 360
QY 361 OTTATTTTAAFRVKNKPLGPAGSENEIPTHVLPNCANIQAOKLKSNSVSGSTHCLSDSD 420
DB 361 OTTATTTTAAFRVKNKPLGPAGSENEIPTHVLPNCANIQAOKLKSNSVSGSTHCLSDSD 420
QY 421 GKDGAGASSHTTTKSMAPPSCSLSL.PVLM.TALAAALSVSLAETS 468
DB 421 GKDGAGASSHTTTKSMAPPSCSLSL.PVLM.TALAAALSVSLAETS 468
```

```
RESULT 7
US-08-837-199A-2
Sequence 2, Application US/08837199A
Patent No. 6455277
GENERAL INFORMATION:
APPLICANT: FOX, GARY M.
APPLICANT: JING, SHUOIAN
APPLICANT: MEN, DIANZHI
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
FILE REFERENCE: A-401C
CURRENT APPLICATION NUMBER: US/08/837,199A
CURRENT FILING DATE: 1997-04-14
```

```
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 465
; TYPE: PR
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2078)..(2078)
; OTHER INFORMATION: N in position 2078 indicates a position of divergence between dif
; NAME/KEY: misc feature
; LOCATION: (2107)..(2107)
; OTHER INFORMATION: N in position 2107 indicates a position of divergence between dif
; OTHER INFORMATION: ferent receptor clones
; NAME/KEY: misc feature
; LOCATION: (2241)..(2241)
; OTHER INFORMATION: N in position 2241 indicates a position of divergence between dif
; OTHER INFORMATION: ferent receptor clones
; NAME/KEY: misc feature
; LOCATION: (2250)..(2250)
; OTHER INFORMATION: N in position 2250 indicates a position of divergence between dif
; OTHER INFORMATION: ferent receptor clones
; NAME/KEY: misc feature
; LOCATION: (2256)..(2294)
; OTHER INFORMATION: N in positions 2256 to 2294 indicates positions of divergence be
; OTHER INFORMATION: tween different receptor clones
; US-08-837-199A-2
```

```
Query Match 93.1%; Score 2316.5; DB 4; Length 465;
Best Local Similarity 92.7%; Pred. No. 2,4e-216;
Matches 434; Conservative 18; Mismatches 13; Indels 3; Gaps 2;
```

```
QY 1 MFLATLYFALPLDLILMSAEVSGDRLDCVKASDQCLKEQSGSTKRTLRQCVAGKETNF 60
DB 1 MFLATLYFALPLDLILMSAEVSGDRLDCVKASDQCLKEQSGSTKRTLRQCVAGKETNF 60
QY 61 SLTSGLEADDECSAMEALKQKSLVNCRCRGKKEKNCRIYMSYQSLQGNDLLEDS 120
DB 61 SLTSGLEADDECSAMEALKQKSLVNCRCRGKKEKNCRIYMSYQSLQGNDLLEDS 120
QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAAKACNLDPTCKKRSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAAKACNLDPTCKKRSAYITPCTT 180
QY 181 SMSNEVCNRRKCHKALRQFPDKVPAGSYGMFCSCRDIACTERRRQTIIVPVCSEYERER 240
DB 181 SVSNDCNRRKCHKALRQFPDKVPAGSYGMFCSCRDIACTERRRQTIIVPVCSEYERER 240
QY 241 PNCLSLQDSCKTNYICRSRLADFTNCOPEBSRSVSNCLKENYADCLLAYSGLIGTWTPN 300
DB 241 PNCLSLQDSCKTNYICRSRLADFTNCOPEBSRSVSNCLKENYADCLLAYSGLIGTWTPN 300
QY 301 YVDSSSLVAWPCDCNSGNDLEDCIKFLNFPKONTCLAKNAIOAFNGSDVTWQAPAPV 360
DB 301 YVDSSSLVAWPCDCNSGNDLEDCIKFLNFPKONTCLAKNAIOAFNGSDVTWQAPAPV 360
QY 361 OTTTATTTTAFRVKPKPLGPAESENEIPTHVLPCCANLQAOQKLSNVSGSTHLCSDSDF 420
DB 361 OTTTATTTTAFRVKPKPLGPAESENEIPTHVLPCCANLQAOQKLSNVSGSTHLCSDSDF 420
QY 421 GKDGLAGASHITTKSMAAPSCSLSLPVLMLTALAALISVLAETS 468
DB 421 EKEGGL-GASSHITTKSMAAPSCSLSLPVLMLTALAALISVLAETS 468
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```
RESULT 8
US-09-388-316C-22
; Sequence 22, Application US/09388316C
```

```
; Patent No. 6777196
; GENERAL INFORMATION:
; APPLICANT: KLEIN, ROBERT D.
; APPLICANT: ROSENTHAL, ARNON
; APPLICANT: HYNES, MARY A.
; TITLE OF INVENTION: NEURTURIN RECEPTOR
; FILE REFERENCE: GENENT.45A2DV1
; CURRENT APPLICATION NUMBER: US/09/388,316C
; CURRENT FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: 09/024,665
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: 60/063,258
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/049,818
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: 60/038,839
; PRIOR FILING DATE: 1997-02-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 465
; TYPE: PR
; ORGANISM: Homo sapiens
; US-09-388-316C-22
```

```
Query Match 93.1%; Score 2316.5; DB 4; Length 465;
Best Local Similarity 92.7%; Pred. No. 2,4e-216;
Matches 434; Conservative 18; Mismatches 13; Indels 3; Gaps 2;
```

```
QY 1 MFLATLYFALPLDLILMSAEVSGDRLDCVKASDQCLKEQSGSTKRTLRQCVAGKETNF 60
DB 1 MFLATLYFALPLDLILMSAEVSGDRLDCVKASDQCLKEQSGSTKRTLRQCVAGKETNF 60
QY 61 SLTSGLEADDECSAMEALKQKSLVNCRCRGKKEKNCRIYMSYQSLQGNDLLEDS 120
DB 61 SLTSGLEADDECSAMEALKQKSLVNCRCRGKKEKNCRIYMSYQSLQGNDLLEDS 120
QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAAKACNLDPTCKKRSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAAKACNLDPTCKKRSAYITPCTT 180
QY 181 SMSNEVCNRRKCHKALRQFPDKVPAGSYGMFCSCRDIACTERRRQTIIVPVCSEYERER 240
DB 181 SVSNDCNRRKCHKALRQFPDKVPAGSYGMFCSCRDIACTERRRQTIIVPVCSEYERER 240
QY 241 PNCLSLQDSCKTNYICRSRLADFTNCOPEBSRSVSNCLKENYADCLLAYSGLIGTWTPN 300
DB 241 PNCLSLQDSCKTNYICRSRLADFTNCOPEBSRSVSNCLKENYADCLLAYSGLIGTWTPN 300
QY 301 YVDSSSLVAWPCDCNSGNDLEDCIKFLNFPKONTCLAKNAIOAFNGSDVTWQAPAPV 360
DB 301 YVDSSSLVAWPCDCNSGNDLEDCIKFLNFPKONTCLAKNAIOAFNGSDVTWQAPAPV 360
QY 361 OTTTATTTTAFRVKPKPLGPAESENEIPTHVLPCCANLQAOQKLSNVSGSTHLCSDSDF 420
DB 361 OTTTATTTTAFRVKPKPLGPAESENEIPTHVLPCCANLQAOQKLSNVSGSTHLCSDSDF 420
QY 421 GKDGLAGASHITTKSMAAPSCSLSLPVLMLTALAALISVLAETS 468
DB 421 EKEGGL-GASSHITTKSMAAPSCSLSLPVLMLTALAALISVLAETS 468
```

```
RESULT 9
US-08-837-199A-12
; Sequence 12, Application us/08837199A
; Patent No. 6455277
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUOJIAN
; APPLICANT: WEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/08/837,199A
```

```

; CURRENT FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 463
; TYPE: PRT
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(539)
; OTHER INFORMATION: No. 64552776= "1 to 539 is -237 to 301 of Figure 5 21bcon"
US-08-837-199A-12

```

```

Query Match          92.9%; Score 2311.5; DB 4; Length 463;
Best Local Similarity 92.9%; Pred. No. 7.2e-216;
Matches 430; Conservative 20; Mismatches 12; Indels 1; Gaps 1;

```

```

QY 1 MFATLYPALPLDLMLSAEYSGDRDLCVASDQCLKEQSCSTKYRTLROCVAGKETNF 60
DB 1 MFATLYPALPLDLMLSAEYSGDRDLCVASDQCLKEQSCSTKYRTLROCVAGKETNF 60
QY 61 SLTSGLEAKDECRSAMEALKOKSLYNCRCKGKMKKCNCLRIYMSYOSLOQNDLLEDS 120
DB 61 SLTSGLEAKDECRSAMEALKOKSLYNCRCKGKMKKCNCLRIYMSYOSLOQNDLLEDS 120
QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHI SKGNCLDAKACNLDDTCKKRSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDVFOQVEHI PKGNCLDAKACNLDDTCKKRSAYITPCTT 180
QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHI PKGNCLDAKACNLDDTCKKRSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDVFOQVEHI PKGNCLDAKACNLDDTCKKRSAYITPCTT 180
QY 181 SMSNEVCNRKCHKALROFPDKVPKHSYGMFCSCRDIACTERRRQTIIVPCSYEERER 240
DB 181 SMSNEVCNRKCHKALROFPDKVPKHSYGMFCSCRDIACTERRRQTIIVPCSYEERER 240
QY 181 SVSNDVCCRKCHKALROFPDKVPKHSYGMFCSCRDIACTERRRQTIIVPCSYEERER 240
DB 181 SVSNDVCCRKCHKALROFPDKVPKHSYGMFCSCRDIACTERRRQTIIVPCSYEERER 240
QY 241 PNCISLQDSCKTNYICRSRLADFTNCPESRSVSNCKENYADCLLAYSGLIGVTMPN 300
DB 241 PNCISLQDSCKTNYICRSRLADFTNCPESRSVSNCKENYADCLLAYSGLIGVTMPN 300
QY 241 PNCISLQDSCKTNYICRSRLADFTNCPESRSVSNCKENYADCLLAYSGLIGVTMPN 300
DB 241 PNCISLQDSCKTNYICRSRLADFTNCPESRSVSNCKENYADCLLAYSGLIGVTMPN 300
QY 301 YVDSLSLVAWCCCSNGNDLEDCIKFTNFKNKNTCLKNAIQAFNGSDVTMMQAPAPV 360
DB 301 YVDSLSLVAWCCCSNGNDLEDCIKFTNFKNKNTCLKNAIQAFNGSDVTMMQAPAPV 360
QY 301 YVDSLSLVAWCCCSNGNDLEDCIKFTNFKNKNTCLKNAIQAFNGSDVTMMQAPAPV 360
DB 301 YVDSLSLVAWCCCSNGNDLEDCIKFTNFKNKNTCLKNAIQAFNGSDVTMMQAPAPV 360
QY 361 OTTATTTTARVKNKPLGPAGSENEIPTHYLPCCANLQAKLKSNVSGTHLCLISNGNY 420
DB 361 OTTATTTTARVKNKPLGPAGSENEIPTHYLPCCANLQAKLKSNVSGTHLCLISNGNY 420
QY 421 GKDGLAGASSHITTKSMAPPSCSLSLPVLMLTALAALLSVS 463
DB 421 GKDGLAGASSHITTKSMAPPSCSLSLPVLMLTALAALLSVS 463
QY 421 EKEGL-GASSHITTKSMAPPSCSLSLPVLMLTALAALLSVS 463
DB 421 EKEGL-GASSHITTKSMAPPSCSLSLPVLMLTALAALLSVS 463

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RESULT 10
US-08-861-990-8
; Sequence 8, Application US/08861990
; Patent No. 6696259
; GENERAL INFORMATION:
; APPLICANT: Ibanez, Carlos F.
; APPLICANT: Arumae, Umas
; APPLICANT: Sarioia, Hannu
; APPLICANT: Suvanto, Petro
; APPLICANT: Trupp, Miles
; APPLICANT: Saarna, Mart
; TITLE OF INVENTION: Glial Cell Line-Derived Neurotrophic Factor Receptors
; FILE REFERENCE: CEPH0418
; CURRENT APPLICATION NUMBER: US/08/861,990
; PRIOR FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: 08/747,842
; PRIOR FILING DATE: 1996-11-13
; PRIOR APPLICATION NUMBER: 60/006,619
; PRIOR FILING DATE: 1995-11-13

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; PRIOR APPLICATION NUMBER: 60/015,767
; PRIOR FILING DATE: 1996-04-16
; PRIOR APPLICATION NUMBER: 60/021,965
; PRIOR FILING DATE: 1996-06-27
; PRIOR APPLICATION NUMBER: 60/020,638
; PRIOR FILING DATE: 1996-06-27
; PRIOR APPLICATION NUMBER: 60/020,639
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-861-990-8

```

```

Query Match          92.9%; Score 2310.5; DB 4; Length 465;
Best Local Similarity 92.5%; Pred. No. 9e-216;
Matches 433; Conservative 18; Mismatches 14; Indels 3; Gaps 2;

```

```

QY 1 MFATLYPALPLDLMLSAEYSGDRDLCVASDQCLKEQSCSTKYRTLROCVAGKETNF 60
DB 1 MFATLYPALPLDLMLSAEYSGDRDLCVASDQCLKEQSCSTKYRTLROCVAGKETNF 60
QY 61 SLTSGLEAKDECRSAMEALKOKSLYNCRCKGKMKKCNCLRIYMSYOSLOQNDLLEDS 120
DB 61 SLTSGLEAKDECRSAMEALKOKSLYNCRCKGKMKKCNCLRIYMSYOSLOQNDLLEDS 120
QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHI SKGNCLDAKACNLDDTCKKRSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDVFOQVEHI SKGNCLDAKACNLDDTCKKRSAYITPCTT 180
QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHI PKGNCLDAKACNLDDTCKKRSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDVFOQVEHI PKGNCLDAKACNLDDTCKKRSAYITPCTT 180
QY 181 SMSNEVCNRKCHKALROFPDKVPKHSYGMFCSCRDIACTERRRQTIIVPCSYEERER 240
DB 181 SMSNEVCNRKCHKALROFPDKVPKHSYGMFCSCRDIACTERRRQTIIVPCSYEERER 240
QY 181 SVSNDVCCRKCHKALROFPDKVPKHSYGMFCSCRDIACTERRRQTIIVPCSYEERER 240
DB 181 SVSNDVCCRKCHKALROFPDKVPKHSYGMFCSCRDIACTERRRQTIIVPCSYEERER 240
QY 241 PNCISLQDSCKTNYICRSRLADFTNCPESRSVSNCKENYADCLLAYSGLIGVTMPN 300
DB 241 PNCISLQDSCKTNYICRSRLADFTNCPESRSVSNCKENYADCLLAYSGLIGVTMPN 300
QY 241 PNCISLQDSCKTNYICRSRLADFTNCPESRSVSNCKENYADCLLAYSGLIGVTMPN 300
DB 241 PNCISLQDSCKTNYICRSRLADFTNCPESRSVSNCKENYADCLLAYSGLIGVTMPN 300
QY 301 YVDSLSLVAWCCCSNGNDLEDCIKFTNFKNKNTCLKNAIQAFNGSDVTMMQAPAPV 360
DB 301 YVDSLSLVAWCCCSNGNDLEDCIKFTNFKNKNTCLKNAIQAFNGSDVTMMQAPAPV 360
QY 301 YVDSLSLVAWCCCSNGNDLEDCIKFTNFKNKNTCLKNAIQAFNGSDVTMMQAPAPV 360
DB 301 YVDSLSLVAWCCCSNGNDLEDCIKFTNFKNKNTCLKNAIQAFNGSDVTMMQAPAPV 360
QY 361 OTTATTTTARVKNKPLGPAGSENEIPTHYLPCCANLQAKLKSNVSGTHLCLISNGNY 420
DB 361 OTTATTTTARVKNKPLGPAGSENEIPTHYLPCCANLQAKLKSNVSGTHLCLISNGNY 420
QY 421 GKDGLAGASSHITTKSMAPPSCSLSLPVLMLTALAALLSVS 468
DB 421 GKDGLAGASSHITTKSMAPPSCSLSLPVLMLTALAALLSVS 468
QY 421 EKEGL-GASSHITTKSMAPPSCSLSLPVLMLTALAALLSVS 465
DB 421 EKEGL-GASSHITTKSMAPPSCSLSLPVLMLTALAALLSVS 465

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RESULT 11
US-08-837-199A-6
; Sequence 6, Application US/08837199A
; Patent No. 6455277
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUOJIAN
; APPLICANT: WEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/08/837,199A
; PRIOR FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 465

```

```

; TYPE: PRT
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (184)..(184)
; OTHER INFORMATION: The 'Xaa' at location 184 stands for Lys, or Asn.
; NAME/KEY: misc feature
; LOCATION: (1)..(510)
; OTHER INFORMATION: note="1 to 510 is -237 to 272 of Fig 5 Hegr-21bf"
; NAME/KEY: misc feature
; LOCATION: (1)..(539)
; OTHER INFORMATION: note="1 to 539 is -237 to 301 of Fig 5 Gdnfr"
; LOCATION: (2078)..(2078)
; OTHER INFORMATION: N in position 2078 indicates a position of divergence between dif
; OTHER INFORMATION: ferent receptor clones
; NAME/KEY: misc feature
; LOCATION: (2256)..(2294)
; OTHER INFORMATION: N in positions 2256 to 2294 indicates positions of divergence bet
; OTHER INFORMATION: ween different receptor clones
; NAME/KEY: misc feature
; LOCATION: (1091)..(1091)
; OTHER INFORMATION: N in position 1091 indicates any nucleic acid
; US-08-837-199A-6

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```

Query Match          92.8%; Score 2309.5; DB 4; Length 465;
Best Local Similarity 92.5%; Pred. No. 1.1e-215;
Matches 433; Conservative 18; Mismatches 14; Indels 3; Gaps 2;

```

```

QY 1 MFATATYFALPLDLLMSAEVSGDRDVCVKSADQCKEOSTKRYTRLQCVAGKETNF 60
DB 1 MFATATYFALPLDLLMSAEVSGDRDVCVKSADQCKEOSTKRYTRLQCVAGKETNF 60
QY 61 SLTSGLEADECBSAMEALKQKSLVNCRCRGKKEKNCIRIYWSMYOSLQGNLLDSDP 120
DB 61 SLTSGLEADECBSAMEALKQKSLVNCRCRGKKEKNCIRIYWSMYOSLQGNLLDSDP 120
QY 121 YEPVNRSLDIPRAVPFISDVFOQVHEISKGNCLDAKACNDPTCKKRSAYITPCTT 180
DB 121 YEPVNRSLDIPRAVPFISDVFOQVHEISKGNCLDAKACNDPTCKKRSAYITPCTT 180
QY 121 YEPVNRSLDIPRAVPFISDVFOQVHEISKGNCLDAKACNDPTCKKRSAYITPCTT 180
DB 121 YEPVNRSLDIPRAVPFISDVFOQVHEISKGNCLDAKACNDPTCKKRSAYITPCTT 180
QY 181 SMSNEVCNRRKCKHAKLQPFQDVPAKHSYGMLFCSCRDIACTERRRQTIYPVCSYERER 240
DB 181 SMSNEVCNRRKCKHAKLQPFQDVPAKHSYGMLFCSCRDIACTERRRQTIYPVCSYERER 240
QY 241 PNCLSLQDSCKTNYICRSRLADFTFNCQPESSRSVSNCKENYADCLAYSGLIGTWTPN 300
DB 241 PNCLSLQDSCKTNYICRSRLADFTFNCQPESSRSVSNCKENYADCLAYSGLIGTWTPN 300
QY 301 YDSSSLVAAPWCDCNSGNDLEDCIKFLNFFKONTCLKNAIOAFNGSDVTVMQAPAPV 360
DB 301 YDSSSLVAAPWCDCNSGNDLEDCIKFLNFFKONTCLKNAIOAFNGSDVTVMQAPAPV 360
QY 361 QTTTATTTAFAVKNKPLPAGSENEIPTHVLPCCANLQAKLKSXSVSGSTHCLSDSP 420
DB 361 QTTTATTTAFAVKNKPLPAGSENEIPTHVLPCCANLQAKLKSXSVSGSTHCLSDSP 420
QY 421 GKDGLAGASSHITTKSMAAPPCSSLSLPLMLTALAALLSVS 468
DB 421 GKDGLAGASSHITTKSMAAPPCSSLSLPLMLTALAALLSVS 468
QY 421 EKEGL-GASSHITTKSMAAPPCSSLSLPLMLTALAALLSVS 465
DB 421 EKEGL-GASSHITTKSMAAPPCSSLSLPLMLTALAALLSVS 465

```

```

RESULT 12
; US-08-837-199A-10
; Sequence 10, Application US/08837199A
; Patent No. 6455277
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHOUJIAN
; APPLICANT: WEN, DUANZHIT
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/08/837,199A

```

```

; CURRENT FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 463
; TYPE: PRT
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: The 'Xaa' at location 5 stands for Thr, Ala, Pro, or Ser.
; NAME/KEY: misc feature
; LOCATION: (1)..(537)
; OTHER INFORMATION: No. 6455277e= "1 to 537 is -235 to 301 of Figure 5 2lacon"
; NAME/KEY: misc feature
; LOCATION: (550)..(550)
; OTHER INFORMATION: N in position 550 indicates any nucleic acid
; US-08-837-199A-10

```

```

Query Match          92.7%; Score 2306.5; DB 4; Length 463;
Best Local Similarity 92.7%; Pred. No. 2.2e-215;
Matches 429; Conservative 20; Mismatches 13; Indels 1; Gaps 1;

```

```

QY 1 MFATATYFALPLDLLMSAEVSGDRDVCVKSADQCKEOSTKRYTRLQCVAGKETNF 60
DB 1 MFATATYFALPLDLLMSAEVSGDRDVCVKSADQCKEOSTKRYTRLQCVAGKETNF 60
QY 61 SLTSGLEADECBSAMEALKQKSLVNCRCRGKKEKNCIRIYWSMYOSLQGNLLDSDP 120
DB 61 SLTSGLEADECBSAMEALKQKSLVNCRCRGKKEKNCIRIYWSMYOSLQGNLLDSDP 120
QY 121 YEPVNRSLDIPRAVPFISDVFOQVHEISKGNCLDAKACNDPTCKKRSAYITPCTT 180
DB 121 YEPVNRSLDIPRAVPFISDVFOQVHEISKGNCLDAKACNDPTCKKRSAYITPCTT 180
QY 121 YEPVNRSLDIPRAVPFISDVFOQVHEISKGNCLDAKACNDPTCKKRSAYITPCTT 180
DB 121 YEPVNRSLDIPRAVPFISDVFOQVHEISKGNCLDAKACNDPTCKKRSAYITPCTT 180
QY 181 SMSNEVCNRRKCKHAKLQPFQDVPAKHSYGMLFCSCRDIACTERRRQTIYPVCSYERER 240
DB 181 SMSNEVCNRRKCKHAKLQPFQDVPAKHSYGMLFCSCRDIACTERRRQTIYPVCSYERER 240
QY 241 PNCLSLQDSCKTNYICRSRLADFTFNCQPESSRSVSNCKENYADCLAYSGLIGTWTPN 300
DB 241 PNCLSLQDSCKTNYICRSRLADFTFNCQPESSRSVSNCKENYADCLAYSGLIGTWTPN 300
QY 301 YDSSSLVAAPWCDCNSGNDLEDCIKFLNFFKONTCLKNAIOAFNGSDVTVMQAPAPV 360
DB 301 YDSSSLVAAPWCDCNSGNDLEDCIKFLNFFKONTCLKNAIOAFNGSDVTVMQAPAPV 360
QY 361 QTTTATTTAFAVKNKPLPAGSENEIPTHVLPCCANLQAKLKSXSVSGSTHCLSDSP 420
DB 361 QTTTATTTAFAVKNKPLPAGSENEIPTHVLPCCANLQAKLKSXSVSGSTHCLSDSP 420
QY 421 GKDGLAGASSHITTKSMAAPPCSSLSLPLMLTALAALLSVS 463
DB 421 GKDGLAGASSHITTKSMAAPPCSSLSLPLMLTALAALLSVS 463
QY 421 EKEGL-GASSHITTKSMAAPPCSSLSLPLMLTALAALLSVS 462
DB 421 EKEGL-GASSHITTKSMAAPPCSSLSLPLMLTALAALLSVS 462

```

```

RESULT 13
; US-08-802-805D-22
; Sequence 22, Application US/08802805D
; Patent No. 6372453
; GENERAL INFORMATION:
; APPLICANT: Robert D. Klein
; TITLE OF INVENTION: Neurturin Receptor
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California

```


COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,805D
FILING DATE: 18-Feb-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 460 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-802-805D-22

Query Match 91.6%; Score 2278; DB 3; Length 460;
Best Local Similarity 91.7%; Pred. No. 1.3e-212;
Matches 429; Conservative 18; Mismatches 13; Indels 8; Gaps 3;

QY 1 MFATLYPALDLILMSAEVSGGDRIDCVKASDQCKECSSTKYRTLRQCVAGKETNF 60
DB 1 MFATLYPALDLILMSAEVSGGDRIDCVKASDQCKECSSTKYRTLRQCVAGKETNF 60
QY 61 SLTSGLEAKDCRSAMEALKOKSLYNCRCKRMKEKNCRIYMSVYOSLGNDLLEDS 120
DB 61 SLTSGLEAKDCRSAMEALKOKSLYNCRCKRMKEKNCRIYMSVYOSLGNDLLEDS 120
QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDCTCKYRSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDCTCKYRSAYITPCTT 180
QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDCTCKYRSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDCTCKYRSAYITPCTT 180
QY 181 SMSNEVCNRRCKHAKLQFQPKVPAKSYGMFCSCRDIACTERRRQTIIVPCSYEERER 240
DB 181 SMSNEVCNRRCKHAKLQFQPKVPAKSYGMFCSCRDIACTERRRQTIIVPCSYEERER 240
QY 176 SVSNDVCNRRCKHAKLQFQPKVPAKSYGMFCSCRDIACTERRRQTIIVPCSYEERER 235
DB 176 SVSNDVCNRRCKHAKLQFQPKVPAKSYGMFCSCRDIACTERRRQTIIVPCSYEERER 235
QY 241 PNCISLSDSCSTNYICSRSLADFTNCOPESSVSNCLKENYADCLAYSGLIGVTWTPN 300
DB 241 PNCISLSDSCSTNYICSRSLADFTNCOPESSVSNCLKENYADCLAYSGLIGVTWTPN 300
QY 236 PNCISLSDSCSTNYICSRSLADFTNCOPESSVSNCLKENYADCLAYSGLIGVTWTPN 295
DB 236 PNCISLSDSCSTNYICSRSLADFTNCOPESSVSNCLKENYADCLAYSGLIGVTWTPN 295
QY 301 YVDSSLSVAPWCDCSNGNDLEDCLEFLNFKONTCLKNAIOAFNGSDVTWMPAPPV 360
DB 301 YVDSSLSVAPWCDCSNGNDLEDCLEFLNFKONTCLKNAIOAFNGSDVTWMPAPPV 360
QY 296 YIDSSLSVAPWCDCSNGNDLEDCLEFLNFKONTCLKNAIOAFNGSDVTWMPAPPV 355
DB 296 YIDSSLSVAPWCDCSNGNDLEDCLEFLNFKONTCLKNAIOAFNGSDVTWMPAPPV 355
QY 361 QTTATTTTARVKNKPLGPAGSENEIPTHVLPNCANIOAQKLKSNVSGSTHLCISDSDF 420
DB 361 QTTATTTTARVKNKPLGPAGSENEIPTHVLPNCANIOAQKLKSNVSGSTHLCISDSDF 420
QY 356 QTTATTTTARVKNKPLGPAGSENEIPTHVLPNCANIOAQKLKSNVSGSTHLCISDSDF 415
DB 356 QTTATTTTARVKNKPLGPAGSENEIPTHVLPNCANIOAQKLKSNVSGSTHLCISDSDF 415
QY 421 GKDLGAGSSHITTKSMAPPSCSLPLVLTALALSLAETS 468
DB 421 GKDLGAGSSHITTKSMAPPSCSLPLVLTALALSLAETS 468
QY 416 EKSGEL-GASSHITTKSMAPPSCSLPLVLTALALSLAETS 460
DB 416 EKSGEL-GASSHITTKSMAPPSCSLPLVLTALALSLAETS 460

RESULT 14

US-09-187-906-11
Sequence 11, Application US/09187906
Patent No. 6677135
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
TITLE OF INVENTION: Ret Ligand (Retl) for Stimulating Neural
TITLE OF INVENTION: and Renal Growth
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Biogen, Inc.

STREET: 14 Cambridge Center
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02142
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/187,906
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/07726
FILING DATE: 07-MAY-97
APPLICATION NUMBER: US 60/017,427
FILING DATE: 08-MAY-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,300
FILING DATE: 07-JUN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/021,859
FILING DATE: 16-JUL-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/043,533
FILING DATE: 10-APR-97
ATTORNEY/AGENT INFORMATION:
NAME: Kaplan, Warren A.
REGISTRATION NUMBER: 34,199
REFERENCE/DOCKET NUMBER: A008 PCT CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-679-2400
TELEFAX: 617-679-2838
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 460 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-187-906-11

Query Match 91.6%; Score 2278; DB 4; Length 460;
Best Local Similarity 91.7%; Pred. No. 1.3e-212;
Matches 429; Conservative 18; Mismatches 13; Indels 8; Gaps 3;

QY 1 MFATLYPALDLILMSAEVSGGDRIDCVKASDQCKECSSTKYRTLRQCVAGKETNF 60
DB 1 MFATLYPALDLILMSAEVSGGDRIDCVKASDQCKECSSTKYRTLRQCVAGKETNF 60
QY 61 SLTSGLEAKDCRSAMEALKOKSLYNCRCKRMKEKNCRIYMSVYOSLGNDLLEDS 120
DB 61 SLTSGLEAKDCRSAMEALKOKSLYNCRCKRMKEKNCRIYMSVYOSLGNDLLEDS 120
QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDCTCKYRSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDCTCKYRSAYITPCTT 180
QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDCTCKYRSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDCTCKYRSAYITPCTT 180
QY 181 SMSNEVCNRRCKHAKLQFQPKVPAKSYGMFCSCRDIACTERRRQTIIVPCSYEERER 240
DB 181 SMSNEVCNRRCKHAKLQFQPKVPAKSYGMFCSCRDIACTERRRQTIIVPCSYEERER 240
QY 176 SVSNDVCNRRCKHAKLQFQPKVPAKSYGMFCSCRDIACTERRRQTIIVPCSYEERER 235
DB 176 SVSNDVCNRRCKHAKLQFQPKVPAKSYGMFCSCRDIACTERRRQTIIVPCSYEERER 235
QY 241 PNCISLSDSCSTNYICSRSLADFTNCOPESSVSNCLKENYADCLAYSGLIGVTWTPN 300
DB 241 PNCISLSDSCSTNYICSRSLADFTNCOPESSVSNCLKENYADCLAYSGLIGVTWTPN 300
QY 236 PNCISLSDSCSTNYICSRSLADFTNCOPESSVSNCLKENYADCLAYSGLIGVTWTPN 295
DB 236 PNCISLSDSCSTNYICSRSLADFTNCOPESSVSNCLKENYADCLAYSGLIGVTWTPN 295
QY 301 YVDSSLSVAPWCDCSNGNDLEDCLEFLNFKONTCLKNAIOAFNGSDVTWMPAPPV 360
DB 301 YVDSSLSVAPWCDCSNGNDLEDCLEFLNFKONTCLKNAIOAFNGSDVTWMPAPPV 360
QY 296 YIDSSLSVAPWCDCSNGNDLEDCLEFLNFKONTCLKNAIOAFNGSDVTWMPAPPV 355
DB 296 YIDSSLSVAPWCDCSNGNDLEDCLEFLNFKONTCLKNAIOAFNGSDVTWMPAPPV 355
QY 361 QTTATTTTARVKNKPLGPAGSENEIPTHVLPNCANIOAQKLKSNVSGSTHLCISDSDF 420
DB 361 QTTATTTTARVKNKPLGPAGSENEIPTHVLPNCANIOAQKLKSNVSGSTHLCISDSDF 420

Db 356 QTTATTTTALRVKKNKPLGPGAGSENEIPTHVLPCCANLQAOXKLSNVSGNTHLCISNGNY 415
 QY 421 GKGLGAGASHITTKSMAAPPSCSLSLPYLMTLTAALISVLAETS 468
 Db 416 EKEGL-GASSHITTKSMAAPPSCSLSLPYLMTLTAALISVLAETS -SLETFS 460

RESULT 15
 US-09-187-906-9
 Sequence 9, Application US/09187906
 Patent No. 6677135
 GENERAL INFORMATION:

APPLICANT: BIOGEN, INC.
 TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Biogen, Inc.
 STREET: 14 Cambridge Center
 CITY: Cambridge
 STATE: MA
 COUNTRY: USA
 ZIP: 02142
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/187,906
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US97/07726
 FILING DATE: 07-MAY-97
 APPLICATION NUMBER: US 60/017,427
 FILING DATE: 08-MAY-96
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/019,300
 FILING DATE: 07-JUN-96
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/021,859
 FILING DATE: 16-JUL-96
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/043,533
 FILING DATE: 10-APR-97
 ATTORNEY/AGENT INFORMATION:
 NAME: Kaplan, Warren A.
 REGISTRATION NUMBER: 34,199
 REFERENCE/DOCKET NUMBER: A008 PCT CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-679-2400
 TELEFAX: 617-679-2838
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 346 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-187-906-9

Query Match 67.8%; Score 1686; DB 4; Length 346;
 Best Local Similarity 89.5%; Pred. No. 2.9e-155;
 Matches 317; Conservative 17; Mismatches 12; Indels 8; Gaps 3;

QY 115 LLEDSYEPNLSRSLDIFRAVPFISDVFOVEHISKGNCLDAKACNLDCTCKYRSAY 174
 Db 1 LLEDSYEPNLSRSLDIFRAVPFIS-----VEHIPKGNCLDAKACNLDCTCKYRSAY 55
 QY 175 ITPECTTSMNSNEVGNRRKCHALROFPDKVPAKHSYGLFCSCRDIACTERRRQTIIVPCS 234
 Db 56 ITPECTTSMNSNDVGNRRKCHALROFPDKVPAKHSYGLFCSCRDIACTERRRQTIIVPCS 115

QY 235 YEERERPNCLSLDSDCKTNYICSRRLADFFTNQPSRSVSNCLXENYADCLLAYSGLIG 294
 Db 116 YEERERPNCLSLDSDCKTNYICSRRLADFFTNQPSRSVSNCLXENYADCLLAYSGLIG 175
 QY 295 TVMTPNYVDSSSLSVAPWCDCSNGNDLEDCLEFNFKDNCTCKXAIQAFNGSDVTW 354
 Db 176 TVMTPNYIDSSSLSVAPWCDCSNGNDLEDCLEFNFKDNCTCKXAIQAFNGSDVTW 235
 QY 355 QPAPVQTTTATTTTAFRVKKNKPLGPGAGSENEIPTHVLPCCANLQAOXKLSNVSGNTHLC 414
 Db 236 QPAPVQTTTATTTTALRVKKNKPLGPGAGSENEIPTHVLPCCANLQAOXKLSNVSGNTHLC 295
 QY 415 LSDSDFGKGLGAGASHITTKSMAAPPSCSLSLPYLMTLTAALISVLAETS 468
 Db 296 ISNGNYEKEGL-GASSHITTKSMAAPPSCSLSLPYLMTLTAALISVLAETS -SLETFS 346

Search completed: February 17, 2005, 09:49:08
 Job time : 28 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 17, 2005, 08:52:13 ; Search time 44 Seconds
(without alignments)
1023.396 Million cell updates/sec

Title: US-10-033-350-2

Perfect score: 2488
Sequence: 1 MFLATLYRALPILDLMSAB.....PVLMLTALNALISVSLAETS 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pirl:*
2: pirl:*
3: pirl:*
4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	505.5	20.3	397 2 JE0082	GPI-linked receptor
2	148	5.9	3051 2 S42373	hypothetical prote
3	131	5.3	2471 2 A49128	cell-fate determin
4	129	5.2	770 2 S04847	leukocyte adhesion
5	129	5.2	2703 1 A24420	notch protein - tr
6	128	5.1	771 2 A45839	leukocyte adhesion
7	127.5	5.1	601 2 B36346	fibulin 1 precursor
8	125.5	5.0	2139 2 A35672	crumbs protein - f
9	125	5.0	965 2 S62935	hypothetical prote
10	123.5	5.0	2195 2 T34264	hypothetical prote
11	121.5	4.9	810 2 T10756	Nel-homolog protei
12	121.5	4.9	886 2 A57172	probable hormone r
13	121	4.9	683 2 C36346	fibulin 1 precursor
14	121	4.9	1292 2 T09229	galactose binding
15	120	4.8	2531 2 T31070	notch homolog - se
16	119.5	4.8	1051 2 J4C091	glycoprotein A - p
17	119.5	4.8	3507 2 T34513	hypothetical prote
18	119	4.8	685 2 S78040	fibulin, splice to
19	119	4.8	705 2 S34968	LDL-receptor-relac
20	119	4.8	4753 1 A47437	major surface glyc
21	117.5	4.7	715 2 J4C222	notch B protein -
22	117	4.7	1203 2 A49175	alpha-2-macroglobu
23	116.5	4.7	4543 1 A53102	GDNF receptor alpa
24	116	4.7	24 2 S69080	notch protein - chlc
25	115.5	4.6	835 2 JP0076	G surface protein
26	115.5	4.6	2704 2 S09118	surface protein ty
27	115	4.6	2395 1 S50820	alpha-5ID immobili
28	114.5	4.6	2533 2 T28675	alpha-5ID-immobil
29	114.5	4.6	2533 2 T28674	alpha-5ID-immobil

30	113	4.5	1599 2 T16210	hypothetical prote
31	111.5	4.5	1722 2 B89753	protein FltC7.4 (l
32	111.5	4.5	2643 2 T29149	hypothetical prote
33	111.5	4.5	2718 2 A23475	G surface protein
34	111	4.5	600 2 S07638	spore coat protein
35	110.5	4.4	907 2 T27317	hypothetical prote
36	110	4.4	2437 2 S42612	transmembrane prot
37	109.5	4.4	5376 2 T42215	zonadhesin - mouse
38	109	4.4	2524 2 A35844	Xotch protein - Af
39	108.5	4.4	1169 2 S38181	filocolution prote
40	108	4.3	1142 2 T30272	hypothetical prote
41	107	4.3	1004 2 J4C221	major surface glyc
42	107	4.3	1296 2 T16859	hypothetical prote
43	106.5	4.3	332 2 T21458	hypothetical prote
44	106.5	4.3	1927 2 G64585	cag pathogenicity
45	106.5	4.3	2233 2 T28669	surface protein 51

ALIGNMENTS

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RESULT 1
JE0082
GPI-linked receptor precursor - mouse
N/Alternate names: GFRalpha-3
C/Species: Mus musculus (house mouse)
C/Date: 21-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C/Accession: JE0082
R/Nomoto, S.; Ito, S.; Yang, L.X.; Ktuchi, K.
Biochem. Biophys. Res. Commun. 244, 849-853, 1998
A/Title: Molecular cloning and expression analysis of GFRalpha-3, a novel CDNA related to
A/Reference number: JE0082; PMID:98205811, PMID:9535755
A/Accession: JE0082
A/Molecule type: mRNA
A/Residues: 1-397 <NOM>
A/Cross-references: UNIPROT:Q35118; DDBJ:AB008833; NID:92627159; PIDD:BA023562.1; PTD:92
C/Comment: This protein plays a distinct role in cell survival and differentiation.
C/Superfamily: Mus musculus GPI-linked receptor
C/Keywords: glycoprotein
F/1-25/Domain: signal sequence #status predicted <SIG>
F/380-397/Region: hydrophobic
F/92,145,306/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      20.3%; Score 505.5; DB 2; Length 397;
Best Local Similarity 35.1%; Pred. No. 2,6e-30;
Matches 125; Conservative 40; Mismatches 148; Indels 43; Gaps 12;

QY 11 PILLDLMSA-----EVSQGDRL-----DVKASDQCLKRSQSCSTKYRTLRQVAKKE 57
DB 10 PLMLTLLVLSLMLPLGAGNSLATENRFVNSCTQARKKCEANPACAAVOHLGSCSTSSLS 69
QY 58 TWFSLTSGLEAKDECSAMEALKOKSLVNCRCRGKKKCNCLRIYWSYQSIQ-GNDLL 116
DB 70 RPLPLESAMSAD-CLEAEQLRNSLIDCRCHRRKQKATCLDIYWTYHAPASLDYEL 128
QY 117 EDSPYE-----PVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAKACNLDTCCKY 170
DB 129 DSPYEDVTYSKPKWKNLSKLMKLP-DSDL-----CLKFMALCTLHDKCDRL 175
QY 171 RSAVITPTCTSMNSNEVCNRRKCHKALROFEDVPAPAGSYGMFCSC--RDIACTERRROT 228
DB 176 RRAYGEAC---SGRCORHLCLAOQRSPFEKAAESHAQGLLCPAPAPDAGGERRRNT 231
QY 229 IYVCSYEERERPNCLSDSCSTNYICSRILADFPFTNOCPSRSVSNCLKENYADCLLA 288
DB 232 IAPSCALPS-VIPNCLDLASFCRADPLGSRMLMDPOTHCHPMD-ILGTATGQ-SRCLRA 288
QY 289 YSGLICTVTPYVVDSSLSVAPWCDCSNGDLEDCLEFLNFKONTCLKAAIOA 344
DB 289 YGLIGTAMTPMIFISKVNTTVALSCTCRGSGNLODECQELERSFSQNPCLVEAIIA 344

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RESULT 2

S42373

hypothetical protein T20G5.3 - *Caenorhabditis elegans*C/Species: *Caenorhabditis elegans*

C/Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-May-2004

C/Accession: S42373

R/Smith, A.

submitted to the EMBL Data Library, March 1994

A/Reference number: S42368

A/Accession: S42373

A/Molecule type: DNA

A/Residues: 1-3051 <SMI>

A/Cross-references: EMBL:Z30423; NID:G458479; PID:G458485

C/Genes: A/Intons: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1;

F/512-679/Domain: von Willebrand factor type A repeat homology <WAL>

F/754-793/Domain: fibronectin type II repeat homology <2FI>

F/1201-1244/Domain: EGF homology <EGF>

Query Match 5.9%; Score 148; DB 2; Length 3051;

Best Local Similarity 18.3%; Pred. No. 0.017;

Matches 97; Conservative 49; Mismatches 158; Indels 226; Gaps 24;

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QY 36 CLKRQSC-STYKRTLRQCV-----AGKTNFSLTSGLEAPDECRSAMEALQ 81
Db 7 CAABAECEETPIGMCCQGVYDVSROHGRPAGVCAVAVNECAEGHDCSSHTCIDT 66
QY 82 KSLYNCRCKRGMKE-----KNCIRIYMSWYQSLQGN-----DLLEDSEYEVN--- 125
Db 67 ADEFTCRCKDSYRDESSDTLKHPRGNVCR-----TVQPRPECDVDSDPMSCDPAKEV 119
QY 126 -----SRLSDIFRAVPFISDVQGVHEHISKANNCLDAKACNLDDTCK 169
Db 120 CIPENVTKKCKANGYSRLP--GRCVVINECEAPRLNCGNAECIDLAEGY-----TC-Q 173
QY 170 YRSAYITPCTTSMNSNEVCNR-----KCHKALRPF- 199
Db 174 CRSGYADISPVQPGRICRAVNECSNKKYVDCSENAICADTEHSYSCRCRPFADVS 233
QY 200 --PKVP-----AKHSYGMIFGSCR----- 217
Db 234 AAFNKLPGRCIEAVNECAPSLDCKNAFCEDKEG--ICRCRPGYVDSNPAARH 290
QY 218 -----DIACTERRRQTIIVPCSYEE-----RERFNC----- 243
Db 291 PGRICTRPEVEXIKTDKTSBSTDGCDBPN-----PKCGANBAVCQHRGNCCEVETA 345
QY 244 -----LSLQDSCKTNYICRSRLADFTNCOPE-----SRSV 274
Db 346 FRYTDGSCRVYASCSKRNKCDKNAICLNRFDSYTCQCRPGYIDLADLTNAPGRICKELI 405
QY 275 SNCKLEN-----YADCLAYGSLGTWTPNRYVD--SSSLVAPKWCDCSNGDLDDCLKF 328
Db 406 NECASSDNECSPYACIDATNGVACQCL--DGFIDVSSRYNKPGRGQCTNNSNECSE--KS 462
QY 329 LNFKDNUTCLKNA-----IOAFNGSDVTVMQAPPVQTTATTT 368
Db 463 L-----NTCDENADCVDTPTDGYTCQCTGCFVDVSSNANLPGRVCTVQTT 507

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RESULT 3

A49128

cell-fate determining gene Notch2 protein - rat

C/Species: *Rattus norvegicus* (Norway rat)

C/Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004

C/Accession: A49128

R/Weinmaster, G.; Roberts, V.J.; Lemke, G.

Development 116, 931-941, 1992

A/Title: Notch2: a second mammalian Notch gene.

A/Reference number: A49128; MUID:93202015; PMID:1295745

A/Accession: A49128

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-2471 <WEI>

A/Cross-references: UNIPROT:Q9GM30

A/Experimental source: Schwann cell

A/Note: sequence extracted from NCBI backbone (NCBI:P127811)

C/Superfamily: Notch protein; ankyrin repeat homology; EGF homology

F/264-235/Domain: EGF homology <EGF1>

F/799-830/Domain: EGF homology <EGF1>

F/877-908/Domain: EGF homology <EGF2>

F/1029-1060/Domain: EGF homology <EGF3>

F/1067-1098/Domain: EGF homology <EGF3>

F/1153-1184/Domain: EGF homology <EGF3>

F/1181-1222/Domain: EGF homology <EGF4>

F/11876-1908/Domain: ankyrin repeat homology <AN1>

F/1909-1941/Domain: ankyrin repeat homology <AN2>

F/1943-1975/Domain: ankyrin repeat homology <AN3>

F/1976-2008/Domain: ankyrin repeat homology <AN4>

F/2009-2041/Domain: ankyrin repeat homology <AN5>

Query Match 5.3%; Score 131; DB 2; Length 2471;

Best Local Similarity 19.8%; Pred. No. 0.25;

Matches 117; Conservative 63; Mismatches 195; Indels 216; Gaps 31;

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QY 23 GGDRLDYCA-----SDCLKEGSCSTKRTLR-----QVAGKTNFSLTSGI 66
Db 1169 GGYRCECPGVGYVNCSEYEDC--QNPCCQNGTCTIDLNVHFKSCSPRG-----TRGL 1220
QY 67 ---FAKDECRSMEALKOKSL-----YNCRCKRGMKEKNCIRIYMSWYQSLQGNLLE 117
Db 1221 LCEENIDDCAGAPHCCLNGGQCVDRIGYSGRCPLGFRGER-----CEG----- 1263
QY 118 DSPYEPVNSRLSDIFRAVPFISDVQGVHEHISKANNCLDAKACNLDDT--CKYRSAYI 175
Db 1264 -----DI-----NECL--SNPCSSSGSLDCTQLKNVQ 1289
QY 176 TPCTTSMN-----EVCNRKRC-----HKALRPFDPVPAKHSYGMIFGSCRDI 219
Db 1290 CVCSAFTGRHCTETFLVCPQKPLNGTCVAVSNVPDGFICRCRPGFSGARCOSSCGOV 1349
QY 220 ACTERRRQTIIVPCSYEERERPNCLSLQDSCKT-----YICRSRLADP 263
Db 1350 KC--RREGQCVHTASGHCPCPNHKDCEGSCASNPCHGTCYPRQRPPIYSGRCSPFFW 1407
QY 264 FTNCQ-----PERSVSNCLKENYADCLAYSGLGTWTPNRYV--DSSSLVAPKWC 314
Db 1408 GSHCESYATPSTPAPCLSGYCAD--KARDGICDEACNSHACOMDGGDSLTMEDPMAN 1465
QY 315 CSNS-----GNLFE-----DCLKTLNF-----FDQNTCLK--NA 341
Db 1466 CTSLRCMEYINNOCDLCTAECT--PDNFEQQRNSYTKCYDKYCADHFDQNDCKGKCN 1524
QY 342 IOAFNGSDVTVMQAP-----APPVQTTATTT-----TAFRVNKKPL 378
Db 1525 EECGMDGLDCAADPBNLABGILVIYVLLPPEQLDQSRFLAALGTLHTNRIRIQDQ 1584
QY 379 G-----PAGSENEIPTHVLPCCANLQAKL--KSNVSGSTHCLSDSD--FG 421
Db 1585 GALMVPYVYGERKAMKKQVARRSLP--DEGQOIIIGSKVLEIDNRQCVDDQCFK 1641
QY 422 KDGLAGA--SSHITTKSMAPPSCLS-----SLPTLMTALAAALLSVL 464
Db 1642 NTDAAMALASHAIOGTLSTPLVSVSESDPRTPLLYLAAVAVIILFL 1692

```

RESULT 4

S04847

leukocyte adhesion protein CD18 precursor - mouse

C/Species: *Mus musculus* (house mouse)

C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004

C/Accession: S04847

R/Wilson, R.W.; O'Brien, W.F.; Beaudet, A.L.

Nucleic Acids Res. 17, 5397, 1989

A/Title: Nucleotide sequence of the cDNA from the mouse leukocyte adhesion protein CD18.

A/Reference number: S04847; MUID:89345112; PMID:2569711

A/Accession: S04847

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 17, 2005, 08:52:13 ; Search time 181 Seconds

(without alignments)
1324.050 Million cell updates/sec

Title: US-10-033-350-2

Perfect score: 2488
Sequence: 1 MPALATYFPLPLDLMSAE.....PVLMLTRALLLSVSLAETS 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2488	100.0	468	1	GFR1_RAT
2	2458	98.8	468	2	O35246
3	2452	98.6	468	1	GFR1_MOUSE
4	2449.5	98.5	463	2	O35748
5	2419.5	97.2	463	2	O35252
6	2316.5	93.1	465	1	GFR1_HUMAN
7	1914.5	76.9	469	1	GFR1_CHICK
8	1548.5	62.2	472	2	O98TT9
9	1453.5	58.4	481	2	O98TT8
10	1158	46.5	225	2	O90WT2
11	1120.5	45.0	464	2	O35977
12	1112.5	44.7	463	1	GFR2_MOUSE
13	1110.5	44.6	463	2	O920V3
14	1109.5	44.6	464	1	GFR2_HUMAN
15	1098.5	44.2	444	2	O792X9
16	1076.5	43.3	465	1	GFR2_CHICK
17	984.5	39.6	431	1	GFR4_CHICK
18	974.5	39.2	495	2	O6T5C3
19	860	34.6	358	2	O922A3
20	792	31.8	331	2	O725E2
21	790	31.8	330	2	O922A2
22	513	20.6	109	2	O8J5G8
23	511	20.5	400	1	GFR3_HUMAN
24	505.5	20.3	397	1	GFR3_MOUSE
25	504	20.3	385	2	O9R2D0
26	504	20.3	397	2	O6AXR3
27	462	18.6	273	1	GFR4_RAT
28	452	18.2	260	1	GFR4_MOUSE
29	388	15.6	239	1	GFR4_HUMAN
30	367.5	14.8	222	2	O9Q2G2
31	214	8.6	394	2	O6UXV0

32	204.5	8.2	393	2	O6SJ00	O6SJ00 mus musculus
33	194.5	7.8	77	2	O91Y87	O91Y87 ratu
34	168	6.8	238	2	O6SJD9	O6SJD9 mus musculus
35	154.5	6.2	502	2	O7QDB4	O7QDB4 anopheles g
36	150	6.0	3183	2	O65ZC2	O65ZC2 caenorhabdi
37	150	6.0	3767	1	MUA3_CAEEL	P34576 caenorhabdi
38	135.5	5.4	814	2	O7R1V1	O7R1V1 giardia lam
39	134.5	5.4	2585	2	O23587	O23587 caenorhabdi
40	131	5.3	2471	1	NTC2_RAT	O9QW30 ratu
41	130.5	5.2	1289	1	O75JU6	O75JU6 dictyoste
42	129.5	5.2	1101	2	O964D2	O964D2 entamoeba h
43	129.5	5.2	1219	1	O95XG5	O95XG5 caenorhabdi
44	129	5.2	771	1	ITB2_MOUSE	P11835 mus musculus
45	129	5.2	2703	1	NOTC_DROME	P07207 drosophila

ALIGNMENTS

RESULT 1	ID	GFR1_RAT	STANDARD;	PRT;	468 AA.
AC	O62997;				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	05-JUL-2004 (Rel. 44, Last annotation update)				
DE	GNF family receptor alpha 1 precursor (GFR-alpha 1) (GNF receptor 1)				
DE	alpha) (GDNFR-alpha) (TGF-beta related neurotrophic factor receptor 1)				
DE	(RET ligand 1)				
GN	Name=gfral; Synonyms=gdnfra, Retl1, Trnr1;				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
ON	NCBI_TaxID=10116;				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Retina;				
RX	MEDLINE=96270513; PubMed=8674117; DOI=10.1016/S0092-8674(00)81311-2;				
RA	Jing S., Wen D., Yu Y., Holst P.L., Luo Y., Fang M., Tamir R.,				
RA	Antonio L., Hu Z., Cupples R., Louis J.-C., Hu S., Altrock B.W.,				
RA	Fox G.M.;				
RT	"GDNF-induced activation of the ret protein tyrosine kinase is				
RT	mediated by GDNFR-alpha, a novel receptor for GDNF.";				
RT	Cell 85:1113-1124(1996).				
RL	[2]				
RP	SEQUENCE FROM N.A.				
RC	SPRAIN=Mistar; TISSUE=Kidney;				
RX	MEDLINE=97332356; PubMed=9177201; DOI=10.1073/pnas.94.12.6238;				
RA	Sanicola M., Hession C.A., Worley D.S., Carmillo P., Ehrenfeld C.,				
RA	Walus L., Robinson S., Jaworski G., Wei H., Tizard R., Whitley A.,				
RA	Papinsky R.B., Cate R.L.;				
RT	"Glial cell line-derived neurotrophic factor-dependent RET activation				
RT	can be mediated by two different cell-surface accessory proteins.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 94:6238-6243(1997).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=96273032; PubMed=8657309; DOI=10.1038/382080a0;				
RA	Treanor J.T.S., Goodman L., de Sauvage F., Stone D.M., Poulsen K.T.,				
RA	Beck C.D., Gray C., Aymann L.P., Pollock R.A., Hefti F.,				
RA	Phillips H.S., Goddard A., Moore M.W., Bui-Bello A., Davies A.M.,				
RA	Arai N., Takahashi M., Vanden R., Henderson C.E., Rosenthal A.;				
RT	"Characterization of a multicomponent receptor for GDNF.";				
RL	Nature 382:80-83(1996).				
CC	- FUNCTION: Receptor for GDNF. Mediates the GDNF-induced				
CC	autophosphorylation and activation of the RET receptor.				
CC	- SUBUNIT: 2 molecules of GDNFR-alpha are thought to form a complex				
CC	with the disulfide-linked GDNF dimer and with 2 molecules of RET.				
CC	- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.				
CC	- TISSUE SPECIFICITY: Expressed in liver, brain and kidney.				
CC	- SIMILARITY: Belongs to the GDNFR family.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -				

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CC -----
 DR EMBL; U93486; AAC52663.1; -.
 DR EMBL; U97142; AAC53300.1; -.
 DR RGD; 2681; Gfrel.
 DR InterPro; IPR003438; GDNF_Receptor.
 DR Pfam; PF02351; GDNF; 1.
 DR PRINTS; PR01316; GDNFRECEPTOR.
 KW Glycoprotein; Gpi-anchor; Lipoprotein; Membrane; Receptor; Signal.
 FT SIGNAL 1 24 Potential.
 FT CHAIN 25 430 GDNF family receptor alpha 1.
 FT PROPEP 431 468 Removed in mature form (Potential).
 FT DOMAIN 362 369 Poly-Thr.
 FT CARBOHYD 59 59 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 347 347 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 406 406 N-linked (GlcNAc...) (Potential).
 FT LIPID 430 430 GPI-anchor amidated serine (Potential).
 SQ SEQUENCE 468 AA; 51649 MW; B2BE5906F5025E0F CRC64;

Query Match 100.0%; Score 2488; DB 1; Length 468;
 Best Local Similarity 100.0%; Pred. No. 2.5e-179;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFLLATYFALPLDLLMSAEVSGGDRDLDCVAKSDQCLKEGSCSTKYRTLRQCVAKETNF 60
 DB 1 MFLLATYFALPLDLLMSAEVSGGDRDLDCVAKSDQCLKEGSCSTKYRTLRQCVAKETNF 60
 QY 61 SLTSGLEAKDCRSAMEALKKOKSLYNCRCKRGKMKCKNCLRIYMSWYOSIQGNDLLEDS 120
 DB 61 SLTSGLEAKDCRSAMEALKKOKSLYNCRCKRGKMKCKNCLRIYMSWYOSIQGNDLLEDS 120
 QY 121 YEPVNSRLSDIFRAVPFISDFVQOYEHISKNNCLDAKACNLDCTCKKRSAYITPCTT 180
 DB 121 YEPVNSRLSDIFRAVPFISDFVQOYEHISKNNCLDAKACNLDCTCKKRSAYITPCTT 180
 QY 181 SMSNEVCNRKCHALRQFPDKVPKASGYMLFSCGDRDIACTERRRQTIIVPCSYEERER 240
 DB 181 SMSNEVCNRKCHALRQFPDKVPKASGYMLFSCGDRDIACTERRRQTIIVPCSYEERER 240
 QY 241 PNCISLQDSCKTNYICRSLADFPNCPQESRSVSNCKENYADCLAYSGIGVTMPN 300
 DB 241 PNCISLQDSCKTNYICRSLADFPNCPQESRSVSNCKENYADCLAYSGIGVTMPN 300
 QY 301 YVDSSSLSVAPWCDCSNGNDLEDCLKPLNPKDNTCLKNALQAFNGSDVTMMQAPPV 360
 DB 301 YVDSSSLSVAPWCDCSNGNDLEDCLKPLNPKDNTCLKNALQAFNGSDVTMMQAPPV 360
 QY 361 OTTATATTTAFAVKKPLPGPAGSENEIPHVLPCANIQAOQLKSNVSGSTHCLSDSPF 420
 DB 361 OTTATATTTAFAVKKPLPGPAGSENEIPHVLPCANIQAOQLKSNVSGSTHCLSDSPF 420
 QY 421 GKDLGAGASHITTKSMAPPSCSLSPLVLMLTALALSLAETS 468
 DB 421 GKDLGAGASHITTKSMAPPSCSLSPLVLMLTALALSLAETS 468

RESULT 2
 ID 035246 PRELIMINARY; PRT: 468 AA.
 AC 035246;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DE GDNF receptor alpha (Glia1 cell line derived neurotrophic factor family receptor alpha 1).
 GN Name=Gfrel; Synonyms=GDNF-alpha;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57; TISSUE=Liver;
 RX MEDLINE=96252741; PubMed=9592044;
 RA Dey B.K., Wong Y.W., Too H.P.;
 RT "Cloning of a novel murine isoform of the glial cell line-derived neurotrophic factor receptor";
 RL Neuroreport 9:37-42(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.L., Feingold E.A., Grouse I.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marubina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pringle C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heltan E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Small D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maita M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory epithelium;
 RA Strausberg R.;
 DR EMBL; AF014117; AAB86599.1; -.
 DR EMBL; BC054378; AAB54378.1; -.
 DR MGD; MGI:1100842; Gfrel.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0019898; C:extrinsic to membrane; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0009653; P:metamorphosis; TAS.
 DR GO; GO:0007399; P:neurogenesis; IMP.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; TAS.
 DR InterPro; IPR003438; GDNF_Receptor.
 DR InterPro; IPR003503; GDNF_Receptor.
 DR Pfam; PF02351; GDNF; 1.
 DR PRINTS; PR01317; GDNFRALPHAL.
 DR PRINTS; PR01316; GDNFRECEPTOR.
 KW RECEPTOR.
 SQ SEQUENCE 468 AA; 51751 MW; 997105C2A6DD6446 CRC64;
 Query Match 98.8%; Score 2458; DB 2; Length 468;
 Best Local Similarity 97.6%; Pred. No. 4.7e-177;
 Matches 457; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFLLATYFALPLDLLMSAEVSGGDRDLDCVAKSDQCLKEGSCSTKYRTLRQCVAKETNF 60
 DB 1 MFLLATYFALPLDLLMSAEVSGGDRDLDCVAKSDQCLKEGSCSTKYRTLRQCVAKETNF 60
 QY 61 SLTSGLEAKDCRSAMEALKKOKSLYNCRCKRGKMKCKNCLRIYMSWYOSIQGNDLLEDS 120
 DB 61 SLTSGLEAKDCRSAMEALKKOKSLYNCRCKRGKMKCKNCLRIYMSWYOSIQGNDLLEDS 120
 QY 121 YEPVNSRLSDIFRAVPFISDFVQOYEHISKNNCLDAKACNLDCTCKKRSAYITPCTT 180
 DB 121 YEPVNSRLSDIFRAVPFISDFVQOYEHISKNNCLDAKACNLDCTCKKRSAYITPCTT 180
 QY 181 SMSNEVCNRKCHALRQFPDKVPKASGYMLFSCGDRDIACTERRRQTIIVPCSYEERER 240
 DB 181 SMSNEVCNRKCHALRQFPDKVPKASGYMLFSCGDRDIACTERRRQTIIVPCSYEERER 240

Db 181. SMSNEVCNRRKCHKALRQFPDKVPAAKHSYGMALFCSGRDVACTERRRQTIIVPVCSEYERER 240
 QY 241 PNCLSLQDSCKTNYICRSRLADFTTNCQPSRSVSNCLKENYADCLAYSGLIGTWTPN 300
 Db 241 PNCLSLQDSCKTNYICRSRLADFTTNCQPSRSVSNCLKENYADCLAYSGLIGTWTPN 300
 QY 301 YUDSSLSVAWPCDCNSGNDLEDCIKFNLFFKONTCLKNAIOAFNGSGSVTMMQAPAPV 360
 Db 301 YUDSSLSVAWPCDCNSGNDLEDCIKFNLFFKONTCLKNAIOAFNGSGSVTMMQAPAPV 360
 QY 361 QTTATTTTAFRYVKNRKLPGAGSENEIPTHVLPCCANLQAOKLKSNVSGSTHCLSDSPD 420
 Db 361 QTTATTTTAFRYVKNRKLPGAGSENEIPTHVLPCCANLQAOKLKSNVSGSTHCLSDNDY 420
 QY 421 GKQGLAGASSHITTKSMAAPPSGSLSLPYMLTALALISVLAETS 468
 Db 421 GKQGLAGASSHITTKSMAAPPSGSLSLPYMLTALALISVLAETS 468

RESULT 3

GFR1_MOUSE STANDARD; PRT; 468 AA.

AC P97785; 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE GDNF family receptor (GFR-alpha 1) (GDNF receptor alpha) (GDNFR-alpha) (TGF-beta related neurotrophic factor receptor 1).

DE Name=Gfral; Synonyms=Gdnfra, Trnrl;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCB1_TaxID=10090;

RP SEQUENCE FROM N.A.

RC TISSUE=Dorsal root ganglion;

RA Matabe K.; (FEB-1997) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Receptor for GDNF. Mediates the GDNF-induced autophosphorylation and activation of the RET receptor (By similarity).

CC -1- SUBUNIT: 2 molecules of GDNFR-alpha are thought to form a complex with the disulfide-linked GDNF dimer and with 2 molecules of RET (By similarity).

CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By similarity).

CC -1- SIMILARITY: Belongs to the GDNFR family.

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CC EMBL; AB000800; BAA19185.1; -

CC MGD; MG1100842; Gfral.

CC InterPro: IPR003438; GDNF_receptor.

CC Pfam: PF02351; GDNF, 1.

CC PRINTS; PR01316; GDNFRRECEPTOR.

CC SIGNAL 1 24 Potential.

CC CHAIN 25 430 GDNF family receptor alpha 1.

CC PROPEP 431 468 Removed in mature form (Potential).

CC DOMAIN 362 369 Thr-rich.

CC CARBOHYD 359 359 N-linked (GlcNAc...) (Potential).

CC CARBOHYD 347 347 N-linked (GlcNAc...) (Potential).

CC CARBOHYD 406 406 N-linked (GlcNAc...) (Potential).

CC CARBOHYD 430 430 GPI-anchor amidated serine (Potential).

CC LIPID 430 430

CC SEQUENCE 468 AA; 51782 MW; AAB393177307212 CRC64;

Query Match 98.6%; Score 2452; DB 1; Length 468;
 Best Local Similarity 97.4%; Pred. No. 1.3e-176;
 Matches 456; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFATATYFALPLDLMSAEVSGDRLDCVKASDQCLKEQSCSTKRTTLRQCVAGKETNF 60
 Db 1 MFATATYFALPLDLMSAEVSGDRLDCVKASDQCLKEQSCSTKRTTLRQCVAGKETNF 60
 QY 61 SLTSGLEADECRAEALKQKSLVNCRCRCKGKKKCNCLRIYWSYQSLQGNLLEDS 120
 Db 61 SLTSGLEADECRAEALKQKSLVNCRCRCKGKKKCNCLRIYWSYQSLQGNLLEDS 120
 QY 121 YEVNRLSDIFRAVPIGDVPOVNHISGNNCLDAACNLDPPCKKRSAYITPCTT 180
 Db 121 YEVNRLSDIFRAVPIGDVPOVNHISGNNCLDAACNLDPPCKKRSAYITPCTT 180
 QY 181 SMSNEVCNRRKCHKALRQFPDKVPAAKHSYGMALFCSGRDVACTERRRQTIIVPVCSEYERER 240
 Db 181 SMSNEVCNRRKCHKALRQFPDKVPAAKHSYGMALFCSGRDVACTERRRQTIIVPVCSEYERER 240
 QY 241 PNCLSLQDSCKTNYICRSRLADFTTNCQPSRSVSNCLKENYADCLAYSGLIGTWTPN 300
 Db 241 PNCLSLQDSCKTNYICRSRLADFTTNCQPSRSVSNCLKENYADCLAYSGLIGTWTPN 300
 QY 301 YUDSSLSVAWPCDCNSGNDLEDCIKFNLFFKONTCLKNAIOAFNGSGSVTMMQAPAPV 360
 Db 301 YUDSSLSVAWPCDCNSGNDLEDCIKFNLFFKONTCLKNAIOAFNGSGSVTMMQAPAPV 360
 QY 361 QTTATTTTAFRYVKNRKLPGAGSENEIPTHVLPCCANLQAOKLKSNVSGSTHCLSDSPD 420
 Db 361 QTTATTTTAFRYVKNRKLPGAGSENEIPTHVLPCCANLQAOKLKSNVSGSTHCLSDNDY 420
 QY 421 GKQGLAGASSHITTKSMAAPPSGSLSLPYMLTALALISVLAETS 468
 Db 421 GKQGLAGASSHITTKSMAAPPSGSLSLPYMLTALALISVLAETS 468

RESULT 4

ID 035748 PRELIMINARY; PRT; 463 AA.

AC 035748; 01-JAN-1998 (T-EMBLrel. 05, Created)

DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)

DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

DE GDNFR-alpha/Trnrl-delta protein.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCB1_TaxID=10116;

RP SEQUENCE FROM N.A.

RC STRAIN=Hannover;

RA Zhong J.; Annies M.; Heumann R.;

RU Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.

CC EMBL; A002072; CAA05171.1; -

CC PIR; S69080; S69080.

CC GO; GO:0004872; F:receptor activity; IEA.

CC InterPro: IPR003438; GDNF_receptor.

CC Pfam: PF02351; GDNF, 1.

CC PRINTS; PR01317; GDNFRALPHA1.

CC PRINTS; PR01316; GDNFRRECEPTOR.

CC SEQUENCE 463 AA; 51032 MW; CCC9583ACE7353CA CRC64;

Query Match 98.5%; Score 2449.5; DB 2; Length 463;
 Best Local Similarity 98.9%; Pred. No. 2e-176;
 Matches 463; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 MFATATYFALPLDLMSAEVSGDRLDCVKASDQCLKEQSCSTKRTTLRQCVAGKETNF 60
 Db 1 MFATATYFALPLDLMSAEVSGDRLDCVKASDQCLKEQSCSTKRTTLRQCVAGKETNF 60
 QY 61 SLTSGLEADECRAEALKQKSLVNCRCRCKGKKKCNCLRIYWSYQSLQGNLLEDS 120
 Db 61 SLTSGLEADECRAEALKQKSLVNCRCRCKGKKKCNCLRIYWSYQSLQGNLLEDS 120

Db	61	SITSGLAEADBEGRSANEALAKOSLYNCRCKRGKKKEKNCRIITMSYQSLQGNDLLEDSP	120
QY	121	YEPVNSRLSDIFRPAVFIISDVFOQVEHISKANNCLDAKACNLDDTCRTKRSAYITPCTT	180
Db	121	YEPVNSRLSDIFRPAVFIISDVFOQVEHISKANNCLDAKACNLDDTCRTKRSAYITPCTT	175
QY	181	SMSNEVCNRKCKHAKLROFFDKVPAGHSGYMLFCSGRDIACTERRROTIVPVCSYEERER	240
Db	176	SMSNEVCNRKCKHAKLROFFDKVPAGHSGYMLFCSGRDIACTERRROTIVPVCSYEERER	235
QY	241	PNCLSLQDSCKTNYICRSRLADFTTNCQPEBSVSNCLEKNVADCLIAYSGLLIGYWTPN	300
Db	236	PNCLSLQDSCKTNYICRSRLADFTTNCQPEBSVSNCLEKNVADCLIAYSGLLIGYWTPN	295
QY	301	YDSSSLSLVAIPWCDGSCGNDLEDCKLPINFADONTCLKNAIOAFNGSGVYTMOPAPV	360
Db	296	YDSSSLSLVAIPWCDGSCGNDLEDCKLPINFADONTCLKNAIOAFNGSGVYTMOPAPV	355
QY	361	QTTTATTTTAFYKVKNPGLGPAEGENEIPTHVLPCCANLQAKUKLSVNSGSTHLCLSDSDF	420
Db	356	QTTTATTTTAFYKVKNPGLGPAEGENEIPTHVLPCCANLQAKUKLSVNSGSTHLCLSDSDF	415
QY	421	GMDGLAGASHTTYSMAAPPGCSLSLSPVLMTLTAALLSVSLAETS	468
Db	416	GMDGLAGASHTTYSMAAPPGCSLSLSPVLMTLTAALLSVSLAETS	463

ID	035252	PRELIMINARY;	PRT;	463 AA.
AC	035252;			
DT	01-JAN-1998	(TREMBLrel. 05, Created)		
DT	01-JAN-1998	(TREMBLrel. 05, Last sequence update)		
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)		
DE	GNMF receptor beta.			
GN	GNMF=Grflr; Synonyms=GNMFR-beta;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57;			
RX	MEDLINE=96252741; PubMed=9592044;			
RA	Dey B. K., Wong Y.W., Too H.P.;			
RT	"Cloning of a novel murine isoform of the glial cell line-derived			
RT	neurotrophic factor receptor.";			
RL	Neuroreport 9:37-42(1998).			
DR	EMBL; AF015102; AAB86600.1; --			
DR	MED; MGI:1100842; Grflr.			
DR	GO; GO:0005615; C:extracellular space; TAS.			
DR	GO; GO:0019898; C:extrinsic to membrane; TAS.			
DR	GO; GO:0004872; F:receptor activity; TAS.			
DR	GO; GO:0009653; P:morphogenesis; TAS.			
DR	GO; GO:0007339; P:neurogenesis; IMP.			
DR	GO; GO:0007189; P:transmembrane receptor protein tyrosine kin. .; TAS			
DR	InterPro; IPR003438; GDNF_receptor.			
DR	InterPro; IPR003503; GDNF_receptor1.			
DR	Pfam; PF02351; GDNF. 1.			
DR	PRINTS; PRO1317; GDNFRALPH1.			
DR	PRINTS; PRO1316; GDNFRECEPTOR.			
DR	Receptor.			
QO	SEQUENCE 463 AA; 51134 MW; EAF2A1522622C037 CRC64;			

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Query Match Similarity 97.2% Score 2419.5 DB 2 Length 463;
Best Local Similarity 96.6% Pred. No. 3 7e-174)
Matches 452; Conservative 8; Mismatches 3; Indels 5; Gaps 1.

QY 1 MFATATYALPLDILMSAEVSGSRDLDCVKASDQCIKQSGSTKYRTTRQCAAKENF 60
    |||||
Db 1 MFATATYVLPDLDDILMSAEVSGSRDLDCVKASDQCIKQSGSTKYRTTRQCAAKENF 60

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QY	6	SLTSLGAEADCEGSAHEALOKSLYNCCCKGKKEKXCLRIYMSWYOSLOQNDLLEDS	120
Db	61	SLTSLGAEADCEGSAHEALOKSLYNCCCKGKKEKXCLRIYMSWYOSLOQNDLLEDS	120
QY	121	YEPVNSRLSDIFRAVVFISDVFOQVEYEHISKGNCLDAKACNLDTCKYRSAYITPCTT	160
Db	121	YEPVNSRLSDIFRAVVFIS-----YEHISKGNCLDAKACNLDTCKYRSAYITPCTT	175
QY	181	SMSEVNCNRKCKHAKALROFPDKVPKASHGYMLFCGCRDIACERRRQTIYPVCSYERER	240
Db	176	SMSEVNCNRKCKHAKALROFPDKVPKASHGYMLFCGCRDVACERRRQTIYPVCSYERER	235
QY	241	PNCLSLQDSCKTYNIRSRSLDFPNNCOPESHRSVNCLEKENYARCLAYSGLGITWTPN	300
Db	236	PNCNLNODSCKTYNIRSRSLDFPNNCOPESHRSVNCLEKENYARCLAYSGLGITWTPN	295
QY	301	YVDSSSLVAPMWCDCSNGNDLEDCLEKFNFPKONTCLKAKAIOAFGNGSDVTMMOPAPV	360
Db	296	YVDSSSLVAPMWCDCSNGNDLEDCLEKFNFPKONTCLKAKAIOAFGNGSDVTMMOPAPV	355
QY	361	QTTATTTATTAFRVKNKPLGAPAGSENIPTHVLPCANIOAKLSNVSGSTHCLSDSDF	420
Db	356	QTTATTTATTAFRKNKPLGAPAGSENIPTHVLPCANIOAKLSNVSGSTHCLSDNDY	415
QY	421	GKXGLAGASHITTKSMAAPSCGSSLSLPLVMLTALALLSVSLAETS	468
Db	416	GKXGLAGASHITTKSMAAPSCGSSLSLPLVVFALALLSVSLAETS	463

RESULT 6			
ID	GPR1_HUMAN	STANDARD;	PRT; 465 AA.
AC	PS5159; 015507; 043912;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	GNDF family receptor alpha 1 precursor (GFR-alpha 1) (GNDF receptor alpha) (GDNFR-alpha) (TGF-beta related neurotrophic factor receptor 1) (RET ligand 1).		
DE	Name=GFR1; Synonyms=GDNFRA, RETL1, TRNR1;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM 1).		
RC	TISSUE=Substantia nigra;		
RX	MEDLINE=96270513; PubMed=8674117; DOI=10.1016/S0092-8674(00)81311-2;		
RA	Uting S., Men D., Yu Y., Holst P.L., Luo Y., Huang M., Tamar R.,		
RA	Antonio L., Hu Z., Cupples R., Louis J.-C., Hu S., Altkork B.W.,		
RA	Fox G.M.;		
RT	"GNF-induced activation of the ret protein tyrosine kinase is		
RT	mediated by GDNFR-alpha, a novel receptor for GDNF.";		
RL	Cell 85:1113-1124(1996).		
RN	[2]		
RP	SEQUENCE FROM N.A. (ISOFORM 2).		
RC	TISSUE=Kidney;		
RX	MEDLINE=97323356; PubMed=9177201; DOI=10.1073/pnas.94.12.6238;		
RA	Sanicola M., Hsahon C.A., Worley D.S., Carmilio P., Ehrenfels C.,		
RA	Walus L., Robinson S., Jaworski G., Wei H., Tizard R., Whitty A.,		
RA	Peplinsky R.B., Cate R.L.;		
RT	"Glial cell line-derived neurotrophic factor-dependent RET activation		
RT	can be mediated by two different cell-surface accessory proteins.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 94:6238-6243(1997).		
RN	[3]		
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS ASN-85 AND ALA-366.		
RX	MEDLINE=98207251; PubMed=9555641; DOI=10.1006/geno.1997.5191;		
RA	Asgritt M., Jing S., Bolt S., Bentley K., Nallaamy S., Halushka M.,		
RA	Fox G.M., Chakravarti A.;		
RT	"Human GFR1: cloning, mapping, genomic structure, and evaluation as a		
RT	candidate gene for Hirschprung disease susceptibility.";		
RL	Genomics 48:354-362 (1998).		
RN	[4]		

SEQUENCE FROM N.A. (ISOFORM 1).
 TISSUE=Thyroid carcinoma;
 MEDLINE=9820874; PubMed=9600247;
 RA Sheldahl S.E., Khorana S., Schultz P.N., Huang E., Thobe N.,
 Hu Z.J., Fox G.M., Jing S., Cote G.J., Gage R.F.;
 RA "Molecular analysis of the GDNF/RET-GDNF-alpha signaling complex in
 RT a kindred with vesicoureteral reflux.";
 RL Hum. Genet. 102:474-478(1998).
 RN (5)
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Substantia nigra;
 RA Hishiki T., Kondoh K., Ichimiya S., Mimura Y., Seki N., Ozaki T.,
 RA Sakiyama S., Takahashi H., Ohnuma N., Tanabe M., Fujimura S.,
 RA Nakagawa A.;
 RT "GDNF-induced differentiation and its enhancement by retinoic acid in
 RT primary human neuroblastomas expressing c-Ret and GDNF-alpha.";
 RL Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.
 RN (6)
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie H.,
 RA Diatchenko U., Mariani K., Farmer A.A., Rubin G.M., Hong J.,
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uday T.B., Tothiyuki S., Abramson R.D., Mullen S.J.,
 RA Raha S.S., Loughran N.A., Peters G.J., McKernan K.J., Gharatne P.H.,
 RA Bosak S.A., McManus P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hults S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smilins D.E.,
 RA Scherch A., Schein J.E., Jones S.U.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN (7)
 RP SPLICING ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
 RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
 RA Hillman R.T., Green R.E., Brenner S.E.;
 RT "An unappreciated role for RNA surveillance.";
 RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
 RN (8)
 RP VARIANTS ALA-366 AND ARG-371.
 RX PubMed=14566559; DOI=10.1007/s00439-003-1036-z;
 RA Sasaki A., Kanao M., Kijima K., Akaba K., Hashimoto M., Hasegawa H.,
 RA Otsaki S., Koizumi T., Kureda S., Ogawa Y., Tsuchiya K., Yamamoto W.,
 RA Nakamura T., Hayasaka K.;
 RT "Molecular analysis of congenital central hypoventilation syndrome.";
 RL Hum. Genet. 114:22-26(2003).
 CC -1- FUNCTION: Receptor for GDNF. Mediates the GDNF-induced
 CC autophosphorylation and activation of the RET receptor (By
 CC similarity).
 CC -1- SUBUNIT: 2 molecules of GDNF-alpha are thought to form a complex
 CC with the disulfide-linked GDNF dimer and with 2 molecules of RET
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1:
 CC IsoId=P56159-1; Sequence=displayed;
 CC Name=2:
 CC IsoId=P56159-2; Sequence=VSP_001660;
 CC Note=may be produced at very low levels due to a premature stop
 CC codon in the mRNA, leading to nonsense-mediated mRNA decay;
 CC -1- SIMILARITY: Belongs to the GDNF family.

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EMBL; U97144; AAC51646.1; -
 DR EMBL; AF038420; AAC39693.1; -
 DR EMBL; AF038411; AAC39693.1; JOINED.
 DR EMBL; AF038412; AAC39693.1; JOINED.
 DR EMBL; AF038413; AAC39693.1; JOINED.
 DR EMBL; AF038414; AAC39693.1; JOINED.
 DR EMBL; AF038415; AAC39693.1; JOINED.
 DR EMBL; AF038416; AAC39693.1; JOINED.
 DR EMBL; AF038417; AAC39693.1; JOINED.
 DR EMBL; AF038418; AAC39693.1; JOINED.
 DR EMBL; AF038419; AAC39693.1; JOINED.
 DR EMBL; AF038421; AAC39693.1; -
 DR EMBL; AF042080; AAB97371.1; -
 DR EMBL; AF058990; AAC14431.1; -
 DR EMBL; AF058991; AAC14431.1; JOINED.
 DR EMBL; AF058992; AAC14431.1; JOINED.
 DR EMBL; AF058993; AAC14431.1; JOINED.
 DR EMBL; AF058994; AAC14431.1; JOINED.
 DR EMBL; AF058995; AAC14431.1; JOINED.
 DR EMBL; AF058996; AAC14431.1; JOINED.
 DR EMBL; AF058997; AAC14431.1; JOINED.
 DR EMBL; AF058998; AAC14431.1; JOINED.
 DR EMBL; U95847; AAB71811.1; -
 DR EMBL; BC014962; AAB14962.1; -
 DR Gene; HGNC:4243; GFRAL.
 DR H-InvDB; HIX0009233; -
 DR MM; 601496; -
 DR GO; GO:0019898; Cretinism to membrane; NAS.
 DR GO; GO:004672; Fretinism activity; NAS.
 DR GO; GO:0007166; P-cell surface receptor linked signal transdu. .; NAS.
 DR InterPro; IPR003438; GDNF_receptor.
 DR Pfam; PF02351; GDNF; 1.
 DR PRINTS; PR01316; GDNFRECEPTOR.
 DR Alternative splicing; Glycoprotein; GPI-anchor; Lipoprotein; Membrane;
 KW Polymorphism; Receptor; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 429 GDNF family receptor alpha 1.
 FT PROPEP 430 465 Removed in mature form (Potential).
 FT DOMAIN 362 369 Poly-Thr.
 FT CARBOHYD 359 359 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 347 347 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 406 406 N-linked (GlcNAc...) (Potential).
 FT LIPID 429 429 GPI-anchor amidated serine (Potential).
 FT VARSPPLIC 140 144 Missing (in isoform 2).
 FT FTId=VSP_001660.
 FT Y->N (in dbSNP:8192662).
 FT FTId=VAR_012488.
 FT T->A (in dbSNP:2072276).
 FT L->R (may be involved in congenital
 FT central hypoventilation syndrome).
 FT FTId=VAR_018261.
 FT Missing (in Ref. 1).
 FT F->P (in Ref. 1).
 FT CONFLICT 245 245
 FT CONFLICT 358 358
 SQ SEQUENCE 465 AA; 51455 MW; 91A550D06A6777BD CRC64;
 Query Match 93.1%; Score 2316.5; DB 1; Length 465;
 Best Local Similarity 92.7%; Pred. No. 2.2e-166;
 Matches 434; Conservative 18; Mismatches 13; Indels 3; Gaps 2;
 QY 1 MFATATYFALPLDILMSAVSGDRLDCVKASDQCLKQSGCTKYRTLRQCVAGKRTNF 60
 DB 1 MFATATYFALPLDILMSAVSGDRLDCVKASDQCLKQSGCTKYRTLRQCVAGKRTNF 60

QY 61 SLTSGLEAKDECSRAMEALKOKSLYNCRCKRMKKEKNCRLRIYMSYOSLGNDLLEBSP 120
 DB 61 SLTSGLEAKDECSRAMEALKOKSLYNCRCKRMKKEKNCRLRIYMSYOSLGNDLLEBSP 120
 QY 121 YEPNRSRLSDIFRAVPFISDVFOQVEHISKGNCLDAAKACMLDTCCKYRSAYITPCTT 180
 DB 121 YEPNRSRLSDIFRAVPFISDVFOQVEHISKGNCLDAAKACMLDTCCKYRSAYITPCTT 180
 QY 181 SMSNEVCNRKCHKALROFPDVPKPAHSYGMFCSCRDIACTERRRQTIIVPCSYEERER 240
 DB 181 SVSNDVCNRKCHKALROFPDVPKPAHSYGMFCSCRDIACTERRRQTIIVPCSYEERER 240
 QY 241 PNCISLSDSCSKTNYICRSLADFTNCPESRSVSNCKENYADCLLAYSGLIGTWMFN 300
 DB 241 PNCISLSDSCSKTNYICRSLADFTNCPESRSVSNCKENYADCLLAYSGLIGTWMFN 300
 QY 301 YVDSSSSVAPWCCSNGNDLECLKPLNFKDTCCKNAIQARNGSDVTMMQPAFV 360
 DB 301 YVDSSSSVAPWCCSNGNDLECLKPLNFKDTCCKNAIQARNGSDVTMMQPAFV 360
 QY 361 QTTATTTTARVKNKPLGPAGSENEIPTHVLPCCANLQAOGLKSNVSGSTHCLSDSP 420
 DB 361 QTTATTTTARVKNKPLGPAGSENEIPTHVLPCCANLQAOGLKSNVSGSTHCLSDSP 420
 QY 421 GKDGAGASSHITTKSMAAPSCSLSPVLMALTAALSVSLAETS 468
 DB 421 EKESL-GASSHITTKSMAAPSCSLSPVLMALTAALSVSLAETS 465

RESULT 7

GFRL_CHICK STANDARD; PRT; 469 AA.

AC 013156;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE GDNF family receptor alpha 1 precursor (GFR-alpha 1) (GDNF receptor alpha) (GDNFR-alpha) (TGF-beta related neurotrophic factor receptor 1).
 GN Name=GFRAL1; Synonyms=GDNFRA1;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 NC NCB1_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97336104; PubMed=9192899; DOI=10.1038/42729;
 RA Buf-Bello A., Adh J., Pinon L.G.P., Horton A., Thompson J., Rosenthal A., Chinchetru M., Buchman V.L., Davies A.M.;
 RT "Neurturin responsiveness requires a GPI-linked receptor and the Ret receptor tyrosine kinase";
 RL Nature 387:721-724(1997).
 CC -1- FUNCTION: Receptor for GDNF. Mediates the GDNF-induced autophosphorylation and activation of the RET receptor (By similarity).
 CC -1- SUBUNIT: 2 molecules of GDNFR-alpha are thought to form a complex with the disulfide-linked GDNF dimer and with 2 molecules of RET (By similarity).
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By similarity).
 CC -1- SIMILARITY: Belongs to the GDNFR family.
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 CC EMBL, U90541; AAB61570.1; -

DR InterPro; IPR003438; GDNF_receptor.
 DR Pfam; PF02351; GDNF; 1.
 DR PRINTS; PR01316; GDNFRECEPTOR.
 KW Glycoprotein; GPI-anchor; Lipoprotein; Membrane; Receptor; Signal.
 FT SIGNAL 1 27 Potential.
 FT CHAIN 28 430 GDNF family receptor alpha 1.
 FT PROPEP 431 469 Removed in mature form (Potential).
 FT DOMAIN 361 368 Poly-Thr.
 FT CARBOHYD 62 62 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 163 163 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 346 346 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 405 405 N-linked (GlcNAc...) (Potential).
 FT LIPID 430 430 GPI-anchor amidated serine (Potential).
 SQ SEQUENCE 469 AA; 52043 MW; B9DB68D15218AF39 CRC64;

Query Match 76.9%; Score 1914.5; DB 1; Length 469;
 Best Local Similarity 77.7%; Pred. No. 4.6e-136;
 Matches 366; Conservative 42; Mismatches 46; Indels 15; Gaps 8;

QY 1 MELATLYPALDLILMSAEVS---GGDRLDVCVASDQCLKEQSCSTKYRTLRCVAGKE 57
 DB 1 MELATLYPALDLILMSAEVSGLRGDRLDVCVASDQCLKEQSCSTKYRTLRCVAGKE 60
 QY 58 TNFSITSGLEAKDCRSAMEALKOKSLYNCRCKRMKKEKNCRLRIYMSYOSLGNDLLE 117
 DB 61 SNFSRATGLKAEKDECKSAMKOKSLYNCRCKRMKKEKNCRLRIYMSYOSLGNDLLE 120
 QY 118 DSPYEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAAKACMLDTCCKYRSAYIT 176
 DB 121 DSPYEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAAKACMLDTCCKYRSAYIT 175
 QY 177 PCTTSMNEVCNRKCHKALROFPDVPKPAHSYGMFCSCRDIACTERRRQTIIVPCSYE 236
 DB 176 PCTTSMNEVCNRKCHKALROFPDVPKPAHSYGMFCSCRDIACTERRRQTIIVPCSYE 235
 QY 237 EBERNCISLSDSCSKTNYICRSLADFTNCPESRSVSNCKENYADCLLAYSGLIGTV 296
 DB 236 EBERNCISLSDSCSKTNYICRSLADFTNCPESRSVSNCKENYADCLLAYSGLIGTV 295
 QY 297 MTPNVVDSSSSVAPWCCSNGNDLECLKPLNFKDTCCKNAIQARNGSDVTMMQPAFV 356
 DB 296 MTPNVVDSSSSVAPWCCSNGNDLECLKPLNFKDTCCKNAIQARNGSDVTMMQPAFV 355
 QY 357 APVQTTATTTTARVKNKPLGPAGSENEIPTHVLPCCANLQAOGLKSNVSGSTHCL 414
 DB 356 ILPVQTTATTTTARVKNKPLGPAGSENEIPTHVLPCCANLQAOGLKSNVSGSTHCL 413
 QY 415 LSDSPFGDGLAGAS-SHITTKSMAAPSCSLSPVLMALTAALSVSLAETS 463
 DB 414 LNEAIGKDNTPGVSTHISENSFPALPTSPYPTPLMTALSLFLPS 464

RESULT 8

Q98RT9 PRELIMINARY; PRT; 472 AA.

AC 098RT9;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE GDNF family receptor alpha-1a.
 GN Name=gfr1a; Synonyms=gfr1alpha1;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes; Cyprinidae; Danio.
 NC NCB1_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21135398; PubMed=11237470; DOI=10.1006/dbio.2000.0145;
 RA Shepherd I.T., Beattie C.E., Rathe D.W.;
 RT "Functional analysis of zebrafish GDNF";
 RL Dev. Biol. 231:420-435(2001).
 [2]

SEQUENCE FROM N.A.
 RX PubMed=14660438;
 RA Shepherd I.T., Pletsch J., Elworthy S., Keish R.N., Raible D.W.;
 RT "Roles for GFR(alpha)1 receptors in zebrafish enteric nervous system
 development.";
 RL Development 131:241-249(2004).
 DR EMBL: AY436320; AAK1260.2; -.
 DR ZFIN: ZDB-GENE-010226-2; gfr1a.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR InterPro: IPR003438; GDNF_receptor.
 DR pfam: PF02351; GDNF_1.
 DR PRINTS: PR01317; GDNF_ALPHAL.
 DR PRINTS: PR01316; GDNF_RECEPTOR.
 DR RECEPTOR.
 KM SEQUENCE 472 AA; 52742 MW; 7B5B0C436B299C7D CRC64;
 SQ
 Query Match 62.2%; Score 1548.5; DB 2; Length 472;
 Best Local Similarity 62.2%; Pred. No. 1.9e-108;
 Matches 298; Conservative 60; Mismatches 90; Indels 31; Gaps 8;
 QY 1 MFATATYFALPLDLILMSAE--VSGDRLDVCVASDQCKECSCTKYRTLRQCVAGS 57
 DB 1 MFATATYFALPLDLILMSAE--VSGDRLDVCVASDQCKECSCTKYRTLRQCVAGS 60
 QY 58 TNSLTSLGSLKADKDCRSAMEALKOKSLYNCRCKRGMKCKKCLRIYMSYQSLQNDL 117
 DB 61 SNFSMATGMAKDECRVLVDALQKSPLYNCRCKRGMKCKKCLRIYMSYQSLQNDL 120
 QY 118 DSEYEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDCTCKKRSAYITP 177
 DB 121 DSEYEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDCTCKKRSAYITP 176
 QY 178 CTTSMSN-EVGNRRCKHAKALQPFDPKVPKASGYGMLFCSC---RDIACTERRRQITVPVC 233
 DB 177 CTTSMSN-EVGNRRCKHAKALQPFDPKVPKASGYGMLFCSC---RDIACTERRRQITVPVC 236
 QY 234 SYEERERPNCLSLDSCCTNYTCRSRLADFTNCPERSRSVSNCKENYADCLLAYSGL 293
 DB 237 SYEERERPNCLSLDSCCTNYTCRSRLADFTNCPERSRSVSNCKENYADCLLAYSGL 296
 QY 294 GVTMTNPNVYDSSLSVAPMCDSCNSGNDLEDCLKFLNPFKONTCLKNAIOAFGNSDVTM 353
 DB 297 GVTMTNPNVYDSSLSVAPMCDSCNSGNDLEDCLKFLNPFKONTCLKNAIOAFGNSDVTM 356
 QY 354 WQAPAPVQTTATTTATTTAFRVNKKPLGPAGSENEIPTHVLP-----CANLQAOQLKS 405
 DB 357 WQAPAPVQTTATTTATTTAFRVNKKPLGPAGSENEIPTHVLP-----CANLQAOQLKS 416
 QY 406 NVGSGTHLCLSDDFGKDLGAGASHITTSMAAPSCSLSLPVLMTLALALLSYSL 464
 DB 417 NVGSGTHLCLSDDFGKDLGAGASHITTSMAAPSCSLSLPVLMTLALALLSYSL 463
 RESULT 9
 Q98TT8 PRELIMINARY; PRT; 481 AA.
 ID Q98TT8
 AC Q98TT8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE GDNF family receptor alpha-1b.
 GN Name=gfr1b; Synonym=gfr1a1b;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21153398; PubMed=11237470; DOI=10.1006/dbio.2000.0145;
 RA Shepherd I.T., Beattie C.E., Raible D.W.;
 RT "Functional analysis of zebrafish GDNF."

Dev. Biol. 231:420-435(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX PubMed=14660438;
 RA Shepherd I.T., Pletsch J., Elworthy S., Keish R.N., Raible D.W.;
 RT "Roles for GFR(alpha)1 receptors in zebrafish enteric nervous system
 development.";
 RL Development 131:241-249(2004).
 DR EMBL: AY436321; AAK1261.2; -.
 DR ZFIN: ZDB-GENE-010226-3; gfr1b.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR InterPro: IPR003438; GDNF_receptor.
 DR pfam: PF02351; GDNF_1.
 DR PRINTS: PR01316; GDNF_RECEPTOR.
 DR RECEPTOR.
 KM SEQUENCE 481 AA; 53639 MW; 478917653049CE23 CRC64;
 SQ
 Query Match 58.4%; Score 1453.5; DB 2; Length 481;
 Best Local Similarity 59.8%; Pred. No. 2.8e-101;
 Matches 289; Conservative 56; Mismatches 95; Indels 43; Gaps 11;
 QY 1 MFATATYFALPLDLILMSAEV---SGDRLDVCVASDQCKECSCTKYRTLRQCVAG 55
 DB 8 MFATATYFALPLDLILMSAEV---SGDRLDVCVASDQCKECSCTKYRTLRQCVAG 67
 QY 56 KETNESLTSLGSLKADKDCRSAMEALKOKSLYNCRCKRGMKCKKCLRIYMSYQSLQNDL 115
 DB 68 RTNPFMKGPPEAODECRNALISMKOSPLYDCKCRGMKCKKCLRIYMSYQSLQNDL 127
 QY 116 LEDSPYEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDCTCKKRSAYITP 175
 DB 128 LEDSPYEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDCTCKKRSAYITP 183
 QY 176 TPCTTMS-NEVCNRRCKHAKALQPFDPKVPKASGYGMLFCSCRD---IACTEERRRQITVP 231
 DB 184 TPCTTMS-NEVCNRRCKHAKALQPFDPKVPKASGYGMLFCSCRD---IACTEERRRQITVP 243
 QY 232 VCSYERERPNCLSLDSCCTNYTCRSRLADFTNCPERSRSVSNCKENYADCLLAYSGL 291
 DB 244 VCSYERERPNCLSLDSCCTNYTCRSRLADFTNCPERSRSVSNCKENYADCLLAYSGL 303
 QY 292 LGTWTNPNVYDSSLSVAPMCDSCNSGNDLEDCLKFLNPFKONTCLKNAIOAFGNSDVTM 351
 DB 304 LGTWTNPNVYDSSLSVAPMCDSCNSGNDLEDCLKFLNPFKONTCLKNAIOAFGNSDVTM 363
 QY 352 TWMQAPAPVQTTATTTATTTAFRVNKKPLGPAGSENEI--PT-----HVLPCANLQ 399
 DB 364 TWMQAPAPVQTTATTTATTTAFRVNKKPLGPAGSENEI--PT-----HVLPCANLQ 417
 QY 400 AOKLKSNGSGTHLCLSDDFGKDLGAGASH--ITTKSMAAPSCSLSLPVLMTLALALLSYSL 457
 DB 418 AOKLKSNGSGTHLCLSDDFGKDLGAGASH--ITTKSMAAPSCSLSLPVLMTLALALLSYSL 467
 QY 458 ALL 460
 DB 468 STL 470
 RESULT 10
 Q98WK2 PRELIMINARY; PRT; 225 AA.
 ID Q98WK2
 AC Q98WK2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE GDNF receptor alpha (Fragment).
 GN Name=gfr1a;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

Df	InterPro:IPR003504; GDNF_receptorA2.
DR	Pfam: PF02351; GDNF; 1.
DR	PRINTS; PR01318; GDNFRALPHA2.
DR	PRINTS; PR01316; GDNFRECEPTOR.
KW	Receptor.
SQ	SEQUENCE 464 AA; 51668 MW; 81168301BE50D6CC CRC64;
Query Match	45.0%; Score 1120.5; DB 2; Length 464;
Best Local Similarity	47.6%; Pred. No. 3,56-76;
Matches 224;	Conservative 81; Mismatches 139; Indels 27; Gaps 9
Qy	1 MFAT---LYPAL--PLDLLLMSAEVSGD-----RLDCVKASDOCLEQGSCSTKYRTL 49
Dd	1 MILANFLCFEFLIDETLRSLSPSSLSQSEELHGMRPVDVCVRANELCAAESNCSRYRTL 60
Qy	50 RGVAKKENPFLTLTGLLEAKDECSRAMEALKQSKLVNCRCKRMKEKNCLTIYSMYS 109
Dd	61 RQLARDRNTWL-----ANKRCQAALLEVOESPLDYCKRRKMKELCLOIYSHLG 115
Qy	110 L--QGNLLDSFEYPEVNRLSDIFRAVPFISDVYQQVEHSIKNNCLDAKACNLDDTC 168
Dd	116 LTGEFEFYASPYEFVTLSRLSDIFRLASIFSCTGTDPAVTSKSNHCLDAKKCNLNNDCK 175
Qy	169 KRSAYITPTCTTSMG-NEVNCRKCHKALROFPFKPAKSYGMFLFCSCDIACTERERRQ 227
Dd	176 KIRSYISICNEIEIPTSRCKNRKCHKALROFFPRVPSBYTYMLFPCSODDAQERRRQ 235
Qy	228 TIYPVCSYEERPNPCSLSDSCKNYVCRERLADFTNCOPEBSRVSNCLKENYADCIL 287
Dd	236 TLPSCSYDKRKPKCLDLRSICRDHLCNSRLADFLANCRASYRTITSCPADNYOACLG 295
Qy	288 AVSGLIGIVMTENVYDS--SSLVAAPWCDCSNGNLEDCLKLFNFKONTCLKAIQAF 345
Dd	296 SYAGMIGFPMTEINVYDSNPGTGIIVSPMCNCGSGNMEECEKEKLRFDTENPCLRNAIQAF 355
Qy	346 GNQSDVTMGAPAPVQTATTATTTAFRNKNEPLGP--ASEENIIPIHYLPFGCNIQAQCL 403
Dd	356 GNGTDVNMSPKPSLPATQAP----REKTPSLPDLDSDLTSLGSVITTCSTIQEGQL 410
Qy	404 KSNVSGSTHLCLSDSPFKDGLAGASHTTKSMAPAPSCSLSLPLVLMT 454
Dd	411 KANNSELSMCTELTLTINISGSKVIKUNGSSRALSAALVALPLVLMT 461
RESULT 12	
GFR2_MOUSE	
ID	GFR2_MOUSE STANDARD; PRT; 463 AA.
AC	008842;
DT	01-NOV-1997 (Rel. 35, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	GNDF family receptor alpha 2 precursor (GFR-alpha 2) (Neurturin receptor alpha) (NTRN-alpha) (NRTN-alpha) (tGF-beta related neurotrophic factor receptor 2) (GDNF receptor beta) (GDNFR-beta).
NB	Name=Gfr22; Synonyms=Gdnfrb, Trn22;
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxId=10090;
RN	[1]
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX	MEDLINE=9735791; PubMed=9182803; DOI=10.1016/S0896-6273(00)80318-9;
RA	Balch R.H., Tansey M.G., Golden J.P., Creedon D.J., Heuckeroth R.O.,
RA	Keck C.L., Zimonjic D.B., Popescu N.C., Johnson E.W., Jr.,
RA	Malbrandt J.;
RT	"Trn2, a novel receptor that mediates neurturin and GDNF signaling through Ret.";
RT	Neuron 18:793-802(1997).
CC	-!- FUNCTION: Receptor for neurturin. Mediates the NRTN-induced autophosphorylation and activation of the Ret receptor. Also able to mediate GDNF signaling through the Ret tyrosine kinase receptor.
CC	-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By

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CC similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Long;
CC IsoId=008842-1; Sequence=Displayed;
CC Name=2; Synonyms=Short;
CC IsoId=008842-2; Sequence=VSP_001662;
CC -1- TISSUE SPECIFICITY: Neurons of the superior cervical and dorsal
CC root ganglia, and adult brain and testis. Low level in the spleen
CC and in the adrenal gland.
CC -1- SIMILARITY: Belongs to the GDNFR family.
CC -----
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CC -----
CC EMBL; AF002701; AAC53548.1; -.
CC MGD; MGI:1195462; Gfra2.
CC InterPro; IPR003438; GDNF_receptor.
CC Pfam; PF02351; GDNF; 1.
CC PRINTS; PR01316; GDNFRECEPTOR.
CC KW Alternative splicing; Glycoprotein; GPI-anchor; Lipoprotein; Membrane;
CC Receptor; Signal.
CC FT SIGNAL 1 21 Potential.
CC FT CHAIN 22 443 GDNF family receptor alpha 2.
CC FT PROPE 444 463 Removed in mature form (Potential).
CC FT CARBOHYD 52 52 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 357 357 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 413 413 N-linked (GlcNAc...) (Potential).
CC FT LIPID 443 443 GPI-anchor amidated serine (Potential).
CC FT VARSPDIC 14 146 Missing (in isoform 2).
CC FT /Ftrid=VSP_001662.
CC SQ SEQUENCE 463 AA; 51598 MW; 4FBA95F586C61F78 CRC64;

Query Match 44.7%; Score 1112.5; DB 1; Length 463;
Best Local Similarity 47.6%; Pred. No. 1.4e-75;
Matches 224; Conservative 81; Mismatches 139; Indels 27; Gaps 9;

QY 1 MFAT--LYFAL--PLDLLMSAEVSGD-----RLDCVYASDQCLKQSGSTYRTL 49
DB 1 MIANAFCLEFFIDETLRSLASPSPOGSEIHGMRPQVDCVRANIELCAAESNCSRYRTL 60
QY 50 ROCVAGKETNFSLTGLEAKDECRSAMEALKOKSLYNCRCKGKMKKXNCLRIYWSYOS 109
DB 61 RQCLAGRDNTML-----ANKECQALAEVLQESPLDCKCKGKMKELQCLQIYWSIHIG 115
QY 110 L-QGNDLLEDSPYEPVNSRLSDIFRAVPFISDFQOVEHISKGNLCLDAKACNLDDTCK 168
DB 116 LTEGEEFYEASPEYPTSRISDLIFRLASIFSGTADPVVASAKSNHCLDAKACNLNDNCK 175
QY 169 KYRSAYITTCSTMS-NEVCNRRKCHKALROFPDKVPAAHSYGLMFCSCDIACTERRRQ 227
DB 176 KYRSAYITICNREISPTERCNRRKCHKALROFPDRVPSEYTYRMLFCSCODQCAERRRQ 235
QY 228 TIYPVSYERERPNCLSDQCKTNYICRSRLADFTTCOPESRSVSNCLKENYADCLL 287
DB 236 TIIPSCSYEDKEKPNCLDLSLCRTIDHLCRSRLADFHANCRASRYRTITSCPDANYQAICG 295
QY 288 AVSGLIGVTWTPNYVDS--SSLVAPWCDCSNSGNDLEDCLEKFNFKONTCLKNAIOAF 345
DB 296 SYAGMIGFMTPTNYVDSNPTGIIVSPWCNCRSGNNEBECEKFLKDPFTNPCRANAIOAF 355
QY 346 GNSDVTMMOPAPPVQTTATTTTAFVKNKPLGP--ASESENIPTHYLPCANLDAQKL 403
DB 356 GNGTDVNMSPKGP-----TFSATQAPRVEKTPSLPDLSDSTLGSIVITTCISIOEGL 410
QY 404 KSNVSGSTHCLSDSPFGKDLGASGSHITTKSMAAPPCSLSLPLMUTL 454
DB 411 KANSKELSLSCFTBELTTNISPSGSKYIKLYSSGCRARLSTALTAFLMWT 461

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RESULT 13
ID Q920Y3 PRELIMINARY; PRT; 463 AA.
AC Q920Y3;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Gial cell line derived neurotrophic factor family receptor alpha
DE 2.
GN Name=Gfra2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RX MEDLINE=22712886; PubMed=12829325; DOI=10.1016/S0169-328X(03)00169-4;
RA Too H.P.;
RT "Real time PCR quantification of GFRalpha-2 alternatively spliced
RT isoforms in murine brain and peripheral tissues.";
RL Brain Res. Mol. Brain Res. 114:146-153(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Wong Y.W., Too H.P.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF398416; AAK97483.1; -.
DR EMBL; AF398411; AAK97483.1; JOINED.
DR EMBL; AF398412; AAK97483.1; JOINED.
DR EMBL; AF398414; AAK97483.1; JOINED.
DR EMBL; AF398415; AAK97483.1; JOINED.
DR EMBL; AF398413; AAK97483.1; JOINED.
DR GO; GO:0004872; F:receptor activity; IEA.
DR Pfam; PF02351; GDNF; 1.
DR PRINTS; PR01316; GDNFRECEPTOR.
DR PRINTS; PR01316; GDNFRECEPTOR.
KW Receptor.
SQ SEQUENCE 463 AA; 51582 MW; 42FA1EF59975E2C CRC64;

Query Match 44.6%; Score 1110.5; DB 2; Length 463;
Best Local Similarity 47.6%; Pred. No. 2e-75;
Matches 224; Conservative 81; Mismatches 139; Indels 27; Gaps 9;

QY 1 MFAT--LYFAL--PLDLLMSAEVSGD-----RLDCVYASDQCLKQSGSTYRTL 49
DB 1 MIANAFCLEFFIDETLRSLASPSPOGSEIHGMRPQVDCVRANIELCAAESNCSRYRTL 60
QY 50 ROCVAGKETNFSLTGLEAKDECRSAMEALKOKSLYNCRCKGKMKKXNCLRIYWSYOS 109
DB 61 RQCLAGRDNTML-----ANKECQALAEVLQESPLDCKCKGKMKELQCLQIYWSIHIG 115
QY 110 L-QGNDLLEDSPYEPVNSRLSDIFRAVPFISDFQOVEHISKGNLCLDAKACNLDDTCK 168
DB 116 LTEGEEFYEASPEYPTSRISDLIFRLASIFSGTADPVVASAKSNHCLDAKACNLNDNCK 175
QY 169 KYRSAYITTCSTMS-NEVCNRRKCHKALROFPDKVPAAHSYGLMFCSCDIACTERRRQ 227
DB 176 KYRSAYITICNREISPTERCNRRKCHKALROFPDRVPSEYTYRMLFCSCODQCAERRRQ 235
QY 228 TIYPVSYERERPNCLSDQCKTNYICRSRLADFTTCOPESRSVSNCLKENYADCLL 287
DB 236 TIIPSCSYEDKEKPNCLDLSLCRTIDHLCRSRLADFHANCRASRYRTITSCPDANYQAICG 295
QY 288 AVSGLIGVTWTPNYVDS--SSLVAPWCDCSNSGNDLEDCLEKFNFKONTCLKNAIOAF 345
DB 296 SYAGMIGFMTPTNYVDSNPTGIIVSPWCNCRSGNNEBECEKFLKDPFTNPCRANAIOAF 355
QY 346 GNSDVTMMOPAPPVQTTATTTTAFVKNKPLGP--ASESENIPTHYLPCANLDAQKL 403
DB 356 GNGTDVNMSPKGP-----TFSATQAPRVEKTPSLPDLSDSTLGSIVITTCISIOEGL 410

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QY 404 KSNVSGSTHLCISDSDFGKDLGASGSHITTKSMAPPCSSISPLVIMLT 454
 DB 411 KANSKSLKSMCFTELTTNISPSGSKVITLYSGSCARLSTALTAFLPLMT 461

RESULT 14

GFR2_HUMAN STANDARD: PRT; 464 AA.
 ID GFR2_HUMAN
 AC 000451; O15316; O15328;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE GDNF family receptor alpha 2 precursor (GFR-alpha 2) (Neurturin receptor alpha) (NTR-alpha) (NRTN-alpha) (TGF-beta related neurotrophic factor receptor 2) (GDNF receptor beta) (GDNFR-beta) (RET ligand 2).
 DE Name=GFR2; Synonyms=GDNFR, RETL2, TRNR2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxId=9606;
 [1]
 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=97325791; PubMed=9182803; DOI=10.1016/S0896-6273(00)80318-9; Balch R.H., Tansey M.G., Golden J.P., Crendon D.J., Henckeroth R.O., Reck C.L., Zimonjic D.B., Popescu N.C., Johnson E.M. Jr., Milbrandt J.;
 RT "Trnr2, a novel receptor that mediates neurturin and GDNF signaling through Ret.";
 RL Neuron 18:793-802(1997).
 [2]
 SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Fetal brain;
 RX MEDLINE=97402208; PubMed=9259272; DOI=10.1093/mmg/6.8.1267; Svavanto P., Martiovaara K., Lindahl M., Arttue U., Moshnyakov M., Horelli-Kuitunen M., Alirainen M.S., Palotie A., Saxiola H., Saarna M.;
 RT "Cloning, mRNA distribution and chromosomal localisation of the gene for glial cell line-derived neurotrophic factor receptor beta, a homologue to GDNFR-alpha.";
 RL Hum. Mol. Genet. 6:1267-1273(1997).
 [3]
 SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Liver;
 RX MEDLINE=9732356; PubMed=9177201; DOI=10.1073/pnas.94.12.6238; Sanicola M., Hession C.A., Worley D.S., Camillo P., Ehrenfeld C., Walus L., Robinson S., Jaworski G., Wei H., Tizard R., Whitty A., Pepinsky R.B., Cate R.B.;
 RT "Glial cell line-derived neurotrophic factor-dependent RET activation can be mediated by two different cell-surface accessory proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:6238-6243(1997).
 CC -1- FUNCTION: Receptor for neurturin. Mediates the NRTN-induced autophosphorylation and activation of the RET receptor. Also able to mediate GDNF signaling through the RET tyrosine kinase receptor.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Long;
 CC IsoId=000451-1; Sequence=Displayed;
 CC Name=2; Synonyms=Short;
 CC IsoId=000451-2; Sequence=VSP_001661;
 CC -1- SIMILARITY: Belongs to the GDNFR family.
 CC -1- SIMILARITY: Belongs to the GDNFR family.
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 CC -----
 DR EMBL; AF002700; AAC52036.1; -
 DR EMBL; U93703; AAB61922.1; -
 DR EMBL; U97145; AAC51647.1; -
 DR Genew; HGNC:4244; GFR2.
 DR MIM; 601956; -
 DR GO; GO:0019898; C:extrinsic to membrane; TAS.
 DR GO; GO:0016167; F:glial cell line-derived neurotrophic factor . . ; TAS.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . . ; TAS.
 DR InterPro; IPR003438; GDNF_Receptor.
 DR Pfam; PF02351; GDNF; 1.
 DR PRINTS; PR01316; GDNFRCEPTOR.
 DR Alternative splicing; Glycoprotein; GPI-anchor, Lipoprotein, Membrane, Receptor, Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 22 444 GDNF family receptor alpha 2.
 FT PROPE 445 464 Removed in mature form (Potential).
 FT CARBOHYD 52 52 N-linked (GlcNAc . .) (Potential).
 FT CARBOHYD 357 357 N-linked (GlcNAc . .) (Potential).
 FT CARBOHYD 413 413 N-linked (GlcNAc . .) (Potential).
 FT LIPID 444 444 GPI-anchor amidated serine (Potential).
 FT VARSPLIC 14 146 Missing (in isoform 2).
 FT CONFLICT 6 6 /Ftd=VSP_001661.
 FT CONFLICT 462 462 V -> A (in Ref. 3).
 FT SEQUENCE 464 AA; 51558 MW; 8BC604D9530FF21F CRC64;
 SQ

Query Match 44.6%; Score 1109.5; DB 1; Length 464;
 Best Local Similarity 47.9%; Pred. No. 2.4e-75;
 Matches 226; Conservative 76; Mismatches 139; Indels 31; Gaps 10;

QY 1 MFLLATYFALPLD-----LMSAVYSV--GDRLDVCKVAKSDQCKBQSGSTKRTL 49
 DB 1 MILANVFLFFFLBETTLASLPSSLGQPEIHKRPVDCVRAELCAASNGSSKRTIL 60
 QY 50 RQVAGKETNPSLTSGEANDCEKAMBALEKXSLVNCRCRCKGKKEKNCRLRTYMSYQS 109
 DB 61 RQCLAGRRNMTL-----ANKEQALAEVLQESPLVDCRCRCKGKKEKLCGLQITWSTHLG 115
 QY 110 L-QGNDLLESPPEYVNSRLSDITFRVAVFISDVFGQVEHLSKGNCLDAKACMLDPTCK 168
 DB 116 LTEGEFEYASPYEPVTSRLSDIFRLASIFSGTGADPVVAKSHKCLDAKACMLDNCK 175
 QY 169 KYRSAYITPCTTSS--NEVCNRKCHALQFPDKVAKSHYGLFPCSCDICTERRRQ 227
 DB 176 KLRSSYSTCRREISPTERCNRKCHALRQFPDVSEYTRMLFSCDQQAERRRQ 235
 QY 228 TIVPVCSYEERERPNCLSDSCRTNYICSRRLADFTNCQPEBSVSNCLKENYADCLL 287
 DB 236 TILPSCSYDEKKNCLDLRGVCRTHDLCRSRLADFPANCRASQYVITSCPADNYQACLG 295
 QY 288 AYSGLIGVTWTPNYVDS--SLSYAPWCDCSNGNDLEDCLKFLNFKDNTCLKNAIQAF 345
 DB 296 SYAGMIGPDMTPNYVDSPTGIIVSPWCSCGSGMEECEKEFLRDETPENCLRNAIQAF 355
 QY 346 GNGSVYTMQAPAPVQTTATTTAFVAKKELGP--AGSENEPHTVLPFCANLQAK 403
 DB 356 GNGDVNVSPKGFQALQAP-----RVEKTPSLPDLSDSTISGTSVITTCVSDEOGL 410
 QY 404 KSNVSGSTHLCISDSDFGKDLGASGSHITTKS--MAAPSCSISPLVIMLT 453
 DB 411 KANSKSLKSMCF--TELTTNISPSGSKVITLYSGSCARLSTALTAFLPLMT 460

RESULT 15
 0792X9 PRELIMINARY: PRT; 444 AA.
 AC 0792X9;
 DT 05-JUL-2004 (TRENBLREL. 27, Created)
 DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
 DE GDNF receptor-beta (Fragment).

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hippocampus;
 RX MEDLINE=97402208; PubMed=9259272; DOI=10.1093/hmg/6.8.1267;
 RA Suvanto P., Wartiovaara K., Lindahl M., Arumae U., Moshnyakov M.,
 RA Horelli-Kuitunen N., Aliraksinen M.S., Palotie A., Sariola H.,
 RA Saarna M.;
 RT "Cloning, mRNA distribution and chromosomal localisation of the gene
 RT for glial cell line-derived neurotrophic factor receptor beta, a
 RT homologue to GDNFR-alpha.";
 RL Hum. Mol. Genet. 6:1267-1273(1997).
 DR EMBL; AF03825; AAD09310.1; -
 DR GO; GO:004872; F:receptor activity; IEA.
 DR InterPro; IPR003438; GDNF_receptor.
 DR InterPro; IPR003504; GDNF_receptor2.
 DR Pfam; PF02351; GDNF; 1.
 DR PRINTS; PRO1318; GDNFRALPHA2.
 DR PRINTS; PRO1316; GDNFRECEPTOR.
 DR Receptor.
 KM Receptor.
 FT NON TER 444 444
 SQ SEQUENCE 444 AA; 49578 MW; A548644EDB36D5F3 CRC64;

Query Match 44.2%; Score 1098.5; DB 2; Length 444;
 Best Local Similarity 49.3%; Pred. No. 1.5e-74;
 Matches 214; Conservative 74; Mismatches 119; Indels 27; Gaps 9;

QY 1 MFAT---LYFAL-PLDLMSAFVSGD-----RLDVKASDQCKEGSCSTKRTL 49
 DB 1 MILANAFCLFFEDETRLSLASPSLQSGSLHGMRPQVDCVRANELCAESNCSRYRTL 60
 QY 50 ROCVAKETFTSLTSGLEAKDECRSAMKALQKSLVNCRCRGKKEKNCRLTYMSWYOS 109
 DB 61 RQCLARDNRNML-----ANKEQALAEVLAQESPLVDCRCRGMKELOQLYMSIHG 115
 QY 110 L-QGNDLLEDSPYEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCCIDAACNLDTCK 168
 DB 116 LTEGEEFYEASPYEPTYSRLSDIFRLASIFSGTDPBAVSTKSNHCLDAKACNLNDCK 175
 QY 169 KYRSATITCTTSMG-NEVGNRRKCHKALQFPDKVPAAKHSYGMFLCSCRDIACTERRQ 227
 DB 176 KLRSSYISICNREISPTERCNRKCHKALQFPDVPSEYTYMLFPCSCODACABRRQ 235
 QY 228 TIVPVCSYEERBPNCISLQDSCTKNYICRSRLADFFTNCOPESSRSVSNCLKENYADCL 287
 DB 236 TILPSCSYEDKEKNCILDRSLCRTDHLCKSLADPHANCRASRYRTITSCPADNYQACLG 295
 QY 288 AVSGLIGTVMTPNYVDS--SSLSVAPWCDGNSGNDLEDCLKPLNFKDNCTCKNAIQAF 345
 DB 296 SYAGMIGFDMTPNYVDSPNPTGIYVSPWCMCRGSGNMBECEKFLRDPTEHPCLRNAIQAF 355
 QY 346 GNGSDVTMMQAPAPVQTTATTTAFAVKKPLGP--AGSENEIPTHVLPCCANLQAKL 403
 DB 356 GNGTDVNMSPKGSPLATQAP-----RVKTPSLPDDLSDSTSLGTSVITTCISIOEGL 410
 QY 404 KSNVSGSTHCLSD 417
 DB 411 KANNSKELSMCFTE 424

Search completed: February 17, 2005, 09:43:55
 Job time : 186 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 17, 2005, 08:52:14 ; Search time 80 Seconds
(without alignments)
2262.548 Million cell updates/sec

Title: US-10-033-350-2

Perfect score: 2488
Sequence: 1 MFLATLYPALPILDLMSAE.....PYLMTLTAALISVSLAETS 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp19808:*
- 2: geneseqp19908:*
- 3: geneseqp20008:*
- 4: geneseqp20018:*
- 5: geneseqp20028:*
- 6: geneseqp20038:*
- 7: geneseqp20038:*
- 8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2488	100.0	468	2	AAW35334 Rat glial
2	2488	100.0	468	2	AAW27327 Rat glial
3	2488	100.0	468	2	AAW37457 Rat Ret 1
4	2488	100.0	468	2	AAW84164 Glial cel
5	2488	100.0	468	7	ADDD11672 Rat glial
6	2488	100.0	468	7	ADDE60800 Rat Prote
7	2488	100.0	468	7	ADDD46323 Rat Prote
8	2488	100.0	468	8	ADJ58694 Rat Ret1
9	2472	99.4	468	2	AAW92298 Rat GDNFR
10	2316.5	93.1	465	2	AAW35333 Human gl1
11	2316.5	93.1	465	5	ABJ05547 Breast ca
12	2316.5	93.1	465	5	ABJ05547 Breast ca
13	2316.5	93.1	465	7	ADDD11673 Human gl1
14	2316.5	93.1	465	7	ADDD46325 Human Pro
15	2316.5	93.1	465	7	ADDE60802 Human Pro
16	2316.5	93.1	465	7	ADN38766 Cancer/an
17	2311.5	92.9	463	2	AAW84167 GDNFR-ald
18	2309.5	92.8	465	2	AAW84165 GDNFR-ald
19	2306.5	92.7	463	2	AAW84166 GDNFR-ald
20	2306.5	92.7	465	2	AAW92300 Human GDN
21	2278	91.6	460	2	AAW37459 Human Ret
22	2278	91.6	460	3	AAW15175 Human GFR
23	2278	91.6	460	6	ABP97180 Tumour-as
24	2278	91.6	460	8	ADJ58703 Human ret
25	1686	67.8	346	2	AAW37458 Human Ret

26	1686	67.8	346	8	ADJ58701 Human ret
27	1431.5	57.5	294	2	AAW84169 GDNFR-ald
28	1220	49.0	232	2	AAW84168 GDNFR-ald
29	1176.5	47.3	498	2	AAW84183 Consensus
30	1120.5	45.0	464	2	AAW71602 Rat neut
31	1120.5	45.0	464	2	AAW92299 Rat GDNFR
32	1120.5	45.0	464	3	AAW80122 Rat neut
33	1120.5	45.0	464	5	ABJ79036 Rat neut
34	1120.5	45.0	464	5	ABJ09630 Amino aci
35	1120.5	45.0	464	5	AAU79266 Rat neut
36	1120.5	45.0	464	7	ADDD11657 Rat neut
37	1120.5	45.0	464	7	ADDE54591 Rat Prote
38	1120.5	45.0	464	7	ADDE63251 Rat Prote
39	1118.5	45.0	460	2	AAW84181 A GDNFR-a
40	1117.5	44.9	464	2	AAW71601 Human neu
41	1117.5	44.9	464	3	AAW15176 Human GFR
42	1117.5	44.9	464	3	AAW80121 Human neu
43	1117.5	44.9	464	5	ABJ79035 Human neu
44	1117.5	44.9	464	5	ABJ09629 Amino aci
45	1117.5	44.9	464	5	AAU79265 Human neu

ALIGNMENTS

RESULT 1
AAW35334 standard; protein; 468 AA.
AAW35334;

01-MAY-1998 (first entry)

Rat glial cell line-derived neurotrophic factor receptor.

Rat; glial cell line-derived neurotrophic factor; GDNF; receptor; treatment; dopaminergic nerve cell disorder; Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis; diabetes; Huntington's disease; glaucoma; retinal degeneration; hearing loss; gene therapy.

Rattus sp.

WO9740152-A1.

30-OCT-1997.

15-APR-1997; 97WO-US006281.

22-APR-1996; 96US-0015907P.

09-MAY-1996; 96US-0017221P.

14-APR-1997; 97US-00837199.

(AMGE-) AMGEN INC.

Fox GW, Wen D, Jing S;

WPI; 1997-535836/49.

N-PSDB; AAT95297.

Glial cell line derived neurotrophic factor receptor - useful to treat dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's disease.

Claim 1; Page 96-98; 196pp; English.

The present sequence is the rat glial cell line-derived neurotrophic factor (GDNF) receptor, which can be used to treat dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's disease or amyotrophic lateral sclerosis, complications of diabetes and Huntington's disease and (optionally) in combination with GDNF glaucoma, retinal degeneration and hearing loss caused by injury to inner ear sensory neurons. The receptor can also be used to block unwanted GDNF activity; analyse GDNF related

CC molecules and stabilise GDNF in pharmaceutical formulations. Receptor
 CC expressing cells, preferably transfected ex vivo, can be used similarly
 CC by implantation, and the use of the receptor cDNA in gene therapy is also
 CC contemplated. Probes based on the cDNA can be used to identify GDNF
 CC responsive cells and tissues, e.g. to identify patients who would benefit
 CC from GDNF therapy, and abnormalities in receptor expression, and to
 CC isolate molecules that form a complex with the cDNA or are
 CC homologous/cross-reactive with the cDNA. Anti-receptor antibodies,
 CC oligonucleotides derived from the cDNA and animal models that overexpress
 CC the receptor can be used to study the biological function of GDNF,
 CC knockout transgenic animals can be used to detect GDNF dependent neurons
 CC or processes and the antibody can be used in immunoassays for the
 CC receptor. The receptor binds GDNF specifically and with high affinity,
 CC acting as part of a complex that mediates/enhances signal transduction by
 CC GDNF, i.e. increasing dopamine uptake in dopaminergic cells

XX Sequence 468 AA;

Query Match 100.0%; Score 2488; DB 2; Length 468;

Best Local Similarity 100.0%; Pred. No. 4.4e-199; Mismatches 0; Indels 0; Gaps 0;

Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELATLYPALPLDLMSAEVSGGDRDLCVAKSDQCKECSCTKYRTLQCVAKETNF 60
 DB 1 MELATLYPALPLDLMSAEVSGGDRDLCVAKSDQCKECSCTKYRTLQCVAKETNF 60
 QY 61 SLTSGLEAKDCRCRAMEALKOKSLYNCRCKGKMKERKCLRTYMSQSLQGNDDLEDP 120
 DB 61 SLTSGLEAKDCRCRAMEALKOKSLYNCRCKGKMKERKCLRTYMSQSLQGNDDLEDP 120
 QY 121 YEPVNSRLSDIFRAVPIFSDVFOQVEHISKGNCLDAKACNLDCTCKKRSAYITPCTT 180
 DB 121 YEPVNSRLSDIFRAVPIFSDVFOQVEHISKGNCLDAKACNLDCTCKKRSAYITPCTT 180
 QY 181 SMSNEVCNRRCKHAKLRFDPKVPKASGYGMFCSCRDIACTERRRQTIIVPCSYEBER 240
 DB 181 SMSNEVCNRRCKHAKLRFDPKVPKASGYGMFCSCRDIACTERRRQTIIVPCSYEBER 240
 QY 241 PNCISLSDSCNTYICRSLADFPNCGPESRSVSNCLKENYADCLLAVSGLIGVTMPN 300
 DB 241 PNCISLSDSCNTYICRSLADFPNCGPESRSVSNCLKENYADCLLAVSGLIGVTMPN 300
 QY 301 YVDSSTLSVAPWCDCNSGNDLEDCLEKFNPKDNTCKNAIQAFGNSDVTMOPAPPV 360
 DB 301 YVDSSTLSVAPWCDCNSGNDLEDCLEKFNPKDNTCKNAIQAFGNSDVTMOPAPPV 360
 QY 361 QTTTATTTTAAFRVKNKPLGPAGSENEIPTHTVLPICANLQAOKLKSNVSGSTHLCSDSD 420
 DB 361 QTTTATTTTAAFRVKNKPLGPAGSENEIPTHTVLPICANLQAOKLKSNVSGSTHLCSDSD 420
 QY 421 GKDGLAGASHITTKSMAPPSCSLSLPIVMTLTAALLSYLAETS 468
 DB 421 GKDGLAGASHITTKSMAPPSCSLSLPIVMTLTAALLSYLAETS 468

RESULT 2

AAW27327
 ID AAW27327 standard; protein; 468 AA.

XX AC AAW27327;

XX DT 27-APR-1998 (first entry)

XX XX Rat glial cell derived neurotrophic factor receptor alpha.

XX XX Glial cell derived neurotrophic factor receptor alpha; GDNF alpha; GDNF;
 XX rat; kidney disease; glomerulonephritis; therapy.

XX OS Ractus sp.

XX XX Key Location/Qualifiers
 FT Peptide 1..24
 FT label= sig_peptide

FT Domain 25..445
 FT /note= "extracellular domain"
 FT Modified-site 61
 FT /note= "O-glycosylated"
 FT Modified-site 349
 FT /note= "O-glycosylated"
 FT Modified-site 408
 FT /note= "O-glycosylated"
 FT Cleavage-site 428..430
 FT /note= "GPI-anchor cleavage/attachment site"
 FT Domain 446..468
 FT /note= "GPI-attachment site"

PD MO9733912-A2.

PD 18-SEP-1997.

PF 13-MAR-1997; 97WO-US004363.

PR 14-MAR-1996; 96US-00615902.

PR 14-MAR-1996; 96US-00618236.

XX (GETH) GENENTECH INC.

XX Klein RD, Moore MW, Rosenthal A, Ryan AM;

XX MPI: 1997-470819/43.

XX N-PSDB; AAT84975.

PT Isolated glial cell derived neurotrophic factor receptor alpha - useful
 PT to develop products to diagnose and treat associated disorders,
 PT particularly enteric nervous system or kidney disorders.

PS Claim 1; Page 78-79; 100pp; English.

CC This protein comprises full-length rat glial cell derived neurotrophic
 CC factor receptor alpha (GDNF receptor), a novel GPI-linked protein that is a
 CC ligand-binding component of the receptor system for GDNF. Its amino acid
 CC sequence was deduced from an isolated cDNA clone (see AAT84975). The
 CC invention relates to novel uses of GDNF and its receptor. In particular,
 CC it relates to native rat GDNF alpha (see AAW27327), its variants and
 CC soluble derivatives (extracellular domain), chimeric GDNF alpha and
 CC antibodies which bind to the GDNF alpha, including agonist and
 CC neutralising antibodies, as well as various uses for these molecules. It
 CC also relates to assay systems for detecting ligands to GDNF alpha,
 CC systems for studying the physiological role of GDNF, diagnostic
 CC techniques for identifying GDNF-related conditions, methods for
 CC identifying molecules homologous to GDNF alpha, and therapeutic
 CC techniques (claimed) for the treatment of GDNF-related and GDNF alpha-
 CC related conditions, particularly kidney disease associated with
 CC glomerulonephritis and enteric nervous system related disorders.
 CC Transgenic and knockout animals are also claimed

XX Sequence 468 AA;

Query Match 100.0%; Score 2488; DB 2; Length 468;

Best Local Similarity 100.0%; Pred. No. 4.4e-199; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELATLYPALPLDLMSAEVSGGDRDLCVAKSDQCKECSCTKYRTLQCVAKETNF 60
 DB 1 MELATLYPALPLDLMSAEVSGGDRDLCVAKSDQCKECSCTKYRTLQCVAKETNF 60
 QY 61 SLTSGLEAKDCRCRAMEALKOKSLYNCRCKGKMKERKCLRTYMSQSLQGNDDLEDP 120
 DB 61 SLTSGLEAKDCRCRAMEALKOKSLYNCRCKGKMKERKCLRTYMSQSLQGNDDLEDP 120
 QY 121 YEPVNSRLSDIFRAVPIFSDVFOQVEHISKGNCLDAKACNLDCTCKKRSAYITPCTT 180
 DB 121 YEPVNSRLSDIFRAVPIFSDVFOQVEHISKGNCLDAKACNLDCTCKKRSAYITPCTT 180
 QY 181 SMSNEVCNRRCKHAKLRFDPKVPKASGYGMFCSCRDIACTERRRQTIIVPCSYEBER 240
 DB 181 SMSNEVCNRRCKHAKLRFDPKVPKASGYGMFCSCRDIACTERRRQTIIVPCSYEBER 240

DB 181 SMSNEVCNRKCKHAKLROFDFKVPAGHSYGMLEFCSCRDIACTERRRQTIIVPVCSEERER 240
 QY 241 PNCLSLQDSCKTNYICRSRLADFTNCOPEBSRSVSNCLKENYADCLLAYSGLLGTWTPN 300
 DB 241 PNCLSLQDSCKTNYICRSRLADFTNCOPEBSRSVSNCLKENYADCLLAYSGLLGTWTPN 300
 QY 301 YDSSSLSYAPWPCDSCNSGNDLEDCLKFLNFFKDNCTCKNAIOAFNGSVYTMQAPPV 360
 DB 301 YDSSSLSYAPWPCDSCNSGNDLEDCLKFLNFFKDNCTCKNAIOAFNGSVYTMQAPPV 360
 QY 361 OTTATTTTAFRVKKNPLGPAAGSENEIPTHVLPCCANLQAOQKLSNVSGSTHLCSDSD 420
 DB 361 OTTATTTTAFRVKKNPLGPAAGSENEIPTHVLPCCANLQAOQKLSNVSGSTHLCSDSD 420
 QY 421 GKDGLAGASSHITTKSMAAPSCSLSLPVLMTALALSLVLAETS 468
 DB 421 GKDGLAGASSHITTKSMAAPSCSLSLPVLMTALALSLVLAETS 468

RESULT 3
 AAW37457
 ID AAW37457 standard; protein; 468 AA.
 XX
 AC AAW37457;
 XX
 DT 21-MAY-1998 (first entry)
 XX
 DE Rat Ret ligand RetL1.
 XX
 KM Ret ligand; RetL1; receptor; signal transduction; rat; cell growth;
 KM renal cell; hypoxic injury; neurodegeneration; motor neurone disease;
 KM toxic injury; hypoxic injury; nephritis; kidney transplant;
 KM multiple sclerosis; infection; meningitis; myelopathy;
 KM Creutzfeldt-Jakob disease; cranial nerve injury; spinal cord injury;
 KM Down's syndrome; cerebral palsy; Lyme disease; muscular dystrophy;
 KM myasthenia gravis; tumour; therapy.
 XX
 OS Rattus sp.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..24
 FT /label= sig_peptide
 XX
 PN MO9744356-A2.
 XX
 PD 27-NOV-1997.
 XX
 PF 07-MAY-1997; 97WO-US007726.
 XX
 PR 08-MAY-1996; 96US-0017427P.
 PR 07-JUN-1996; 96US-0019300P.
 PR 16-JUL-1996; 96US-0021859P.
 PR 11-APR-1997; 97US-0043533P.
 XX
 PA (Bio) BIOGEN INC.
 XX
 PI Sanicola-Nadel M, Hession C, Cate RL;
 XX
 DR WPI; 1998-018431/02.
 DR N-PSDB; AAV00245.
 XX
 PT New nucleic acid encoding ret receptor ligands and related proteins -
 PT vectors, transformed cells and antibodies, used for promoting cell growth
 PT and improving survival of injured cells, especially renal or nerve cells.
 XX
 PS Claim 2; Page 49-51; 113pp; English.
 XX
 CC This protein comprises rat Ret ligand (RetL1) RetL1, a key component of
 CC the Ret signalling pathway that specifically interacts with Ret receptor
 CC protein, triggering Ret dimerisation and/or autophosphorylation of the
 CC Ret tyrosine kinase domain. The amino acid sequence was deduced from a
 CC cDNA clone (see AAV00245) obtained from a rat embryonic kidney cDNA
 CC expression library. Human RetL1 as well as mouse and human RetL2 and

CC RetL2 sequences have also been identified (see AAW37458-63). Vectors
 CC containing retL1 DNA and prokaryotic or eukaryotic host cells transformed
 CC or transfected with these vectors are claimed, as well as a method for
 CC production of RetL1, its soluble variants (e.g. amino acids 1-434) and
 CC fusion proteins with a toxin, imageable compound or radionuclide. RetL1,
 CC optionally when expressed from vectors in vivo, is used to promote growth
 CC of new tissue and survival of damaged tissue, particularly kidney or
 CC neural tissue. Typical applications are in renal failure, nephritis,
 CC kidney transplants, toxic or hypoxic injury, neurodegeneration, motor
 CC neurone disease, multiple sclerosis, bacterial, viral or prion infections
 CC (e.g. meningitis, myelopathy associated with HIV or Creutzfeldt-Jakob
 CC disease), cranial nerve or spinal cord injury, developmental disorders
 CC such as Down's syndrome and cerebral palsy, or conditions involving the
 CC peripheral nervous system (Lyme disease, muscular dystrophy and
 CC myasthenia gravis). Fusion proteins are used to deliver toxins etc. to
 CC Ret-expressing cells, especially tumours
 XX

SQ Sequence 468 AA;
 Query Match 100.0%; Score 248; DB 2; Length 468;
 Best Local Similarity 100.0%; Pred. No. 4,4e-199;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFPLATYFPLPLDLMSAEVSGDRIDCYKASDOCLKSGSCSTKYRTLRQYAGKETNF 60
 DB 1 MFPLATYFPLPLDLMSAEVSGDRIDCYKASDOCLKSGSCSTKYRTLRQYAGKETNF 60
 QY 61 SLTSGLEADECRAEALQKSLVNCRCRGMKEKNCRIYMSYQSLQGNDLLEDS 120
 DB 61 SLTSGLEADECRAEALQKSLVNCRCRGMKEKNCRIYMSYQSLQGNDLLEDS 120
 QY 121 YEVNRLSDIPRAVPFIDVFOVYHISKNNCLDAACNLDPTCKKRSAYITPCTT 180
 DB 121 YEVNRLSDIPRAVPFIDVFOVYHISKNNCLDAACNLDPTCKKRSAYITPCTT 180
 QY 181 SMSNEVCNRKCKHAKLROFDFKVPAGHSYGMLEFCSCRDIACTERRRQTIIVPVCSEERER 240
 DB 181 SMSNEVCNRKCKHAKLROFDFKVPAGHSYGMLEFCSCRDIACTERRRQTIIVPVCSEERER 240
 QY 241 PNCLSLQDSCKTNYICRSRLADFTNCOPEBSRSVSNCLKENYADCLLAYSGLLGTWTPN 300
 DB 241 PNCLSLQDSCKTNYICRSRLADFTNCOPEBSRSVSNCLKENYADCLLAYSGLLGTWTPN 300
 QY 301 YDSSSLSYAPWPCDSCNSGNDLEDCLKFLNFFKDNCTCKNAIOAFNGSVYTMQAPPV 360
 DB 301 YDSSSLSYAPWPCDSCNSGNDLEDCLKFLNFFKDNCTCKNAIOAFNGSVYTMQAPPV 360
 QY 361 OTTATTTTAFRVKKNPLGPAAGSENEIPTHVLPCCANLQAOQKLSNVSGSTHLCSDSD 420
 DB 361 OTTATTTTAFRVKKNPLGPAAGSENEIPTHVLPCCANLQAOQKLSNVSGSTHLCSDSD 420
 QY 421 GKDGLAGASSHITTKSMAAPSCSLSLPVLMTALALSLVLAETS 468
 DB 421 GKDGLAGASSHITTKSMAAPSCSLSLPVLMTALALSLVLAETS 468

RESULT 4
 AAW84164
 ID AAW84164 standard; protein; 468 AA.
 XX
 AC AAW84164;
 XX
 DT 25-MAR-1999 (first entry)
 XX
 DE Glial cell-line derived neurotrophic factor receptor-alpha protein.
 XX
 KM Rat; glial cell-line derived neurotrophic factor receptor-alpha;
 KM GDNF-alpha; glial cell-line-derived neurotrophic factor; GDNF;
 KM neurotrophin; signal transduction; dopaminergic nerve cell;
 KM Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
 KM neurological disorder; diabetes; glaucoma; sensory neuron;
 KM retinal ganglion cell degeneration; sensory neuropathy; retinopathy;
 KM gene therapy.

```

XX Rattus sp.
OS
XX
FH Key
FT Peptide
FT Protein
FT Region
FT /note= "phosphatidylinositol (GPI) anchorage of the
FT receptor to the cytoplasmic membrane"
XX
XX W09854213-A2.
XX
XX 03-DEC-1998.
XX
XX 27-APR-1998; 98WO-US008486.
XX
XX 30-MAY-1997; 97US-00866354.
XX
XX (AMGE-) AMGEN INC.
XX
XX Fox GM, Jing S, Wen D;
XX
XX WPI; 1999-080806/07.
XX N-PSDB; AAV99311.
XX
XX New Isolated glial cell line-derived neurotrophic factor receptors - used
XX to develop products for treating e.g. improperly functioning dopaminergic
XX nerve cells, Parkinson's disease, Alzheimer's disease or amyotrophic
XX lateral sclerosis.
XX
XX Claim 1; Fig 3A-K; 318pp; English.
XX
XX The present sequence represents a rat glial cell line derived
XX neurotrophic factor receptor-alpha (GDNFR-alpha). The protein is capable
XX of complexing with glial cell line-derived neurotrophic factor (GDNF) and
XX mediating cell response to GDNF. GDNFR-alpha proteins are functionally
XX characterized by the ability to bind GDNF and/or neurturin specifically,
XX and to act as part of a molecular complex which mediates or enhances the
XX signal transduction affects of GDNF and/or neurturin. The proteins can be
XX used for treating improperly functioning dopaminergic nerve cells,
XX Parkinson's disease, Alzheimer's disease or amyotrophic lateral
XX sclerosis. They can also be used for treating neurological disorders
XX associated with diabetes, glaucoma or other diseases and conditions
XX involving retinal ganglion cell degeneration, sensory neuropathy caused
XX by injury to, insults to, or degeneration of, sensory neurons,
XX pathological conditions, or disease or injury-related retinopathies. The
XX products can also be used for detection, diagnosis, drug screening and
XX gene therapy
XX
XX Sequence 468 AA:
SQ

```

```

Query Match 100.0%; Score 2488; DB 2; Length 468;
Best Local Similarity 100.0%; Pred. No. 4,4e-199;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MFLATYFALPLDLMSAEVSGGDRDLCVKASDCLKEQSCSTYRTLRQCVAGKETNF 60
DB 1 MFLATYFALPLDLMSAEVSGGDRDLCVKASDCLKEQSCSTYRTLRQCVAGKETNF 60
QY 61 SLTSGLEKDCRSMELKQSLVNCRCRGMKEKCKLRLYWMSYLSQNDLLEBSP 120
DB 61 SLTSGLEKDCRSMELKQSLVNCRCRGMKEKCKLRLYWMSYLSQNDLLEBSP 120
QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDTCCKYRSAYITPCTT 180
DB 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKGNCLDAKACNLDTCCKYRSAYITPCTT 180
QY 181 SMSNEVCNRKCHALROFPDKVPKHSYGMFCSCRDIACTERRRQITVPCSYEBERER 240
DB 181 SMSNEVCNRKCHALROFPDKVPKHSYGMFCSCRDIACTERRRQITVPCSYEBERER 240

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QY 241 PNCLSLDSCKTNVICSRRLADFTNCOPEBSRVSNCIKENYADCLLAYSGLIGTWTPTN 300
DB 241 PNCLSLDSCKTNVICSRRLADFTNCOPEBSRVSNCIKENYADCLLAYSGLIGTWTPTN 300
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DB 301 YVDSSSLVAPWCDCNSGNDLEDCLEKFLNFKNTCLKNAIQAFNGSDVTMMQAPAPV 360
QY 361 QTTATTTTARVKNKPIGPAGSENEIPTHVLPCCANLQAKLSNVSSTHLCISPSDF 420
DB 361 QTTATTTTARVKNKPIGPAGSENEIPTHVLPCCANLQAKLSNVSSTHLCISPSDF 420
QY 421 GKDGLAGASHITTKSMAPPCSLSLPVLMTALALSVSLAETS 468
DB 421 GKDGLAGASHITTKSMAPPCSLSLPVLMTALALSVSLAETS 468

RESULT 5
ADD11672
ID ADD11672 standard; protein; 468 AA.
XX
XX ADD11672;
XX
XX 01-JAN-2004 (first entry)
XX
XX Rat glial cell line derived factor receptor alpha.
XX
XX Rat; Neurturin receptor alpha; NTNRA1pha; receptor; antiparkinsonian;
XX neurotrophic; neuroprotective; antidiabetic; cytokine; neurotrophic factor;
XX gene therapy; amyotrophic lateral sclerosis; diabetes;
XX Parkinson's disease; Alzheimer's disease;
XX glial cell line derived factor receptor alpha; GDNFRalpha.
XX
XX Rattus norvegicus.
XX
XX Key Location/Qualifiers
XX Peptide 1..24
XX /note= "Signal peptide"
XX Protein 25..468
XX /note= "Mature GDNFRalpha"
XX
XX US2003110525-A1.
XX
XX 12-JUN-2003.
XX
XX 03-FEB-2003; 2003US-00357822.
XX
XX 18-FEB-1997; 97US-0038839P.
XX 09-JUN-1997; 97US-0049818P.
XX 24-OCT-1997; 97US-0063258P.
XX 17-FEB-1998; 98US-0002465S.
XX 01-SEP-1999; 99US-00388316.
XX
XX (KLEI/) KLEIN R D.
XX (ROSE/) ROSENTHAL A.
XX (HYNM/) HYNES M A.
XX
XX Klein RD, Rosenthal A, Hynes MA;
XX WPI; 2003-810859/76.
XX N-PSDB; ADD11671.
XX
XX New human neurturin receptor-alpha polypeptide useful for identifying a
XX compound that binds to or activates it, potentially useful as a
XX therapeutic.
XX
XX Example 1; SEQ ID NO 21; 83bp; English.
XX
XX The invention relates to a polypeptide comprising a sequence that is a
XX human neurturin receptor (NTNR) alpha extracellular domain or an allelic
XX variant or mammalian homologue of NTNRA1pha. Also include are an antibody
XX that specifically binds to NTNRA1pha, an isolated nucleic acid encoding

```

CC NTNralpha, an expression vector comprising the nucleic acid, a host cell
 CC comprising the vector and a non-human transgenic animal which contains
 CC cells that express the nucleic acid to produce NTNralpha, (or which
 CC contains cells having an altered NTNralpha gene). The NTNralpha protein
 CC may comprise mature NTNralpha conjugated with, or fused to, a molecule
 CC which increases its serum half-life (e.g. IgG Fc or an IgG salvage
 CC receptor binding epitope). NTNralpha is used to identify a molecule which
 CC binds to or activates it, to purify a molecule which binds to it and to
 CC modulate a physiological response of a cell to neurotrophin. Soluble
 CC NTNralpha or soluble glial cell line derived factor alpha (GDNFRalpha) is
 CC used for activating Ret on the surface of a cell. An antibody that binds
 CC to NTNralpha is used in a composition that further comprises a cytokine
 CC or a neurotrophic factor. The antibody is also used to determine the
 CC presence of NTNralpha in a test sample. An agonist antibody to NTNralpha
 CC is used for activating NTNralpha in a cell. A nucleic acid encoding
 CC NTNralpha is used to produce NTNralpha by culturing a host cell and
 CC recovering NTNralpha. A nucleic acid that encodes NTNralpha or antisense
 CC nucleic acid that inhibits expression of NTNralpha can be used in gene
 CC therapy. Examples of diseases that can be treated are amyotrophic lateral
 CC sclerosis, diabetes, Parkinson's disease, and Alzheimer's disease. The
 CC present sequence represents rat glial cell line derived factor receptor
 CC alpha (GDNFRalpha).

Query Match 100.0%; Score 2488; DB 7; Length 468;
 Best Local Similarity 100.0%; Pred. No. 4,4e-199;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFATATYFALPLDLMSAEVSGDRLDCYKASDOCLKEOSGCTKRTLRQCVAGKETNF 60
 DB 1 MFATATYFALPLDLMSAEVSGDRLDCYKASDOCLKEOSGCTKRTLRQCVAGKETNF 60
 QY 61 SLTSGLEAKDECSAMEALKOKSLYNCRCRKGKKEKNCRIYWSYOSLQGNLDLEDSP 120
 DB 61 SLTSGLEAKDECSAMEALKOKSLYNCRCRKGKKEKNCRIYWSYOSLQGNLDLEDSP 120
 QY 121 YEPVNSRLSDIFRAVFPISDFVFOVEHISKGNCCLDAAKCNLDCTCKYRSAYITPCTT 180
 DB 121 YEPVNSRLSDIFRAVFPISDFVFOVEHISKGNCCLDAAKCNLDCTCKYRSAYITPCTT 180
 QY 181 SMSNEVCNRRKCKAKALROFPDKYPAKHSYGMFLFCSCGDIACCTERRRQTIYPCVSEYERER 240
 DB 181 SMSNEVCNRRKCKAKALROFPDKYPAKHSYGMFLFCSCGDIACCTERRRQTIYPCVSEYERER 240
 QY 241 PNCLSLQDSCKTNYICRSRLADFTTNCQPSRSVSNCKENYADCLAYSGLIGTWTPTN 300
 DB 241 PNCLSLQDSCKTNYICRSRLADFTTNCQPSRSVSNCKENYADCLAYSGLIGTWTPTN 300
 QY 301 YVDSLSLVAWPCDCNSGNDLEDCLKFLNPFKONTCLKNAIQAFNGSDVTWQAPAPV 360
 DB 301 YVDSLSLVAWPCDCNSGNDLEDCLKFLNPFKONTCLKNAIQAFNGSDVTWQAPAPV 360
 QY 361 OTTATTTTAFRYKKNPLGAPGSENEIPTHVLPCCANLQAKLSNVSGSTHCLSDSD 420
 DB 361 OTTATTTTAFRYKKNPLGAPGSENEIPTHVLPCCANLQAKLSNVSGSTHCLSDSD 420
 QY 421 GKDGLAGASSHITTKSMAAPPSCSLSLPTMLTALALSVSLAETS 468
 DB 421 GKDGLAGASSHITTKSMAAPPSCSLSLPTMLTALALSVSLAETS 468

RESULT 6
 ADE60800 standard; protein; 468 AA.
 ADE60800;
 29-JAN-2004 (first entry)
 Rat Protein Q62997, SEQ ID NO 6712.
 Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 OS Rattus norvegicus.
 XX WO2003016475-A2.
 XX 27-FEB-2003.
 XX 14-AUG-2002; 2002MO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 XX 01-NOV-2001; 2001US-0346382P.
 XX 26-NOV-2001; 2001US-0333347P.
 XX (GENO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 PI Woolf C, D'urso D, Befort K, Costigan M,
 DR WPI; 2003-268312/26.
 DR GENBANK; Q62997.
 XX

New composition comprising two or more isolated polypeptides, useful for
 preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.
 The invention discloses a composition comprising two or more isolated rat
 or human polynucleotides or a polynucleotide which represents a fragment,
 derivative or allelic variation of the nucleic acid sequence. Also
 claimed are a vector comprising the novel polynucleotide, a host cell
 comprising the vector, a method for identifying a nucleotide sequence
 which is differentially regulated in an animal subjected to pain and a
 kit to perform the method, an array, a method for identifying an agent
 that increases or decreases the expression of the polynucleotide sequence
 that is differentially expressed in neuronal tissue of a first animal
 subjected to pain, a method for identifying a compound which regulates
 the expression of a polynucleotide sequence which is differentially
 expressed in an animal subjected to pain, a method for identifying a
 compound that regulates the activity of one or more of the
 polynucleotides, a method for producing a pharmaceutical composition, a
 method for identifying a compound or small molecule that regulates the
 activity in an animal of one or more of the polypeptides given in the
 specification, a method for identifying a compound useful in treating
 pain and a pharmaceutical composition comprising the one or more
 polypeptides or their antibodies. The polynucleotide or the compound that
 modulates its activity is useful for preparing a medicament for treating
 pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
 therapy). The sequence presented is a rat protein (shown in table 2 of
 the specification) which is differentially expressed during pain. Note:
 The sequence data for this patent did not form part of the printed
 specification, but was obtained in electronic form directly from WIPO at
 ftp.wipo.int/pub/published_pct_sequences.

Query Match 100.0%; Score 2488; DB 7; Length 468;
 Best Local Similarity 100.0%; Pred. No. 4,4e-199;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFATATYFALPLDLMSAEVSGDRLDCYKASDOCLKEOSGCTKRTLRQCVAGKETNF 60
 DB 1 MFATATYFALPLDLMSAEVSGDRLDCYKASDOCLKEOSGCTKRTLRQCVAGKETNF 60
 QY 61 SLTSGLEAKDECSAMEALKOKSLYNCRCRKGKKEKNCRIYWSYOSLQGNLDLEDSP 120
 DB 61 SLTSGLEAKDECSAMEALKOKSLYNCRCRKGKKEKNCRIYWSYOSLQGNLDLEDSP 120
 QY 121 YEPVNSRLSDIFRAVFPISDFVFOVEHISKGNCCLDAAKCNLDCTCKYRSAYITPCTT 180
 DB 121 YEPVNSRLSDIFRAVFPISDFVFOVEHISKGNCCLDAAKCNLDCTCKYRSAYITPCTT 180

QY 181 SMSNEVCNRRCKHAKLRQFPDKVPKAGSYGMLFCSGCRDIACTEERRRQTIIVPCSYEERER 240
 Db 181 SMSNEVCNRRCKHAKLRQFPDKVPKAGSYGMLFCSGCRDIACTEERRRQTIIVPCSYEERER 240
 QY 241 PNCISLQDSCKTNYICRSRLADFFTNCPESBSVSNCKENYADCLAYSGLIGVTWTPN 300
 Db 241 PNCISLQDSCKTNYICRSRLADFFTNCPESBSVSNCKENYADCLAYSGLIGVTWTPN 300
 QY 301 YVDSLSLVAWPCDCNSGNDLEDCLKFNFKDNTCLKNAIQAFNGSDVTMMQAPAPV 360
 Db 301 YVDSLSLVAWPCDCNSGNDLEDCLKFNFKDNTCLKNAIQAFNGSDVTMMQAPAPV 360
 QY 361 QTTTATTTTAFRVKXKPLGPAGSENEIPTHVLPCCANIQAQKLKSNVSGSTHCLSDSDF 420
 Db 361 QTTTATTTTAFRVKXKPLGPAGSENEIPTHVLPCCANIQAQKLKSNVSGSTHCLSDSDF 420
 QY 421 GKDLGAGASHITTKSMAPPSCSLSLPIVMTLTAALLSVSLAETS 468
 Db 421 GKDLGAGASHITTKSMAPPSCSLSLPIVMTLTAALLSVSLAETS 468

RESULT 7

ID ADD46323 standard; protein; 468 AA.
 XX ADD46323;

DT 29-JAN-2004 (first entry)

DE Rat Protein Q62997, SEQ ID NO 11998.

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KM chronic constriction injury; CCI; spared nerve injury; SN1; Chung.

XX Rattus norvegicus.

OS WO2003016475-A2.

XX 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX Woolf C, D'Urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

DR GENBANK; Q62997.

XX New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,

CC derivative or allelic variation of the nucleic acid sequence. Also

CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence

CC which is differentially regulated in an animal subjected to pain and a

CC kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence

CC that is differentially expressed in neuronal tissue of a first animal

CC subjected to pain, a method for identifying a compound which regulates

CC the expression of a polynucleotide sequence which is differentially

CC expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SN1) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPD at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 468 AA;

Query Match 100.0%; Score 2488; DB 7; Length 468;
 Best Local Similarity 100.0%; Pred. No. 4,4e-199;
 Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFATLYPALPLDLMSAEVSGGRDLCVAPSDCKEKGSCSTKYRTLRCVAGKETNF 60
 Db 1 MFATLYPALPLDLMSAEVSGGRDLCVAPSDCKEKGSCSTKYRTLRCVAGKETNF 60
 QY 61 SLTSGLEAKDCRSAMEALXKSLYNCRCKRGMKKNCLRIYWSMYQSLQGNLDLSDP 120
 Db 61 SLTSGLEAKDCRSAMEALXKSLYNCRCKRGMKKNCLRIYWSMYQSLQGNLDLSDP 120
 QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAKACNLDLDTCKYRSAYITPCTT 180
 Db 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAKACNLDLDTCKYRSAYITPCTT 180
 QY 181 SMSNEVCNRRCKHAKLRQFPDKVPKAGSYGMLFCSGCRDIACTEERRRQTIIVPCSYEERER 240
 Db 181 SMSNEVCNRRCKHAKLRQFPDKVPKAGSYGMLFCSGCRDIACTEERRRQTIIVPCSYEERER 240
 QY 241 PNCISLQDSCKTNYICRSRLADFFTNCPESBSVSNCKENYADCLAYSGLIGVTWTPN 300
 Db 241 PNCISLQDSCKTNYICRSRLADFFTNCPESBSVSNCKENYADCLAYSGLIGVTWTPN 300
 QY 301 YVDSLSLVAWPCDCNSGNDLEDCLKFNFKDNTCLKNAIQAFNGSDVTMMQAPAPV 360
 Db 301 YVDSLSLVAWPCDCNSGNDLEDCLKFNFKDNTCLKNAIQAFNGSDVTMMQAPAPV 360
 QY 361 QTTTATTTTAFRVKXKPLGPAGSENEIPTHVLPCCANIQAQKLKSNVSGSTHCLSDSDF 420
 Db 361 QTTTATTTTAFRVKXKPLGPAGSENEIPTHVLPCCANIQAQKLKSNVSGSTHCLSDSDF 420
 QY 421 GKDLGAGASHITTKSMAPPSCSLSLPIVMTLTAALLSVSLAETS 468
 Db 421 GKDLGAGASHITTKSMAPPSCSLSLPIVMTLTAALLSVSLAETS 468

RESULT 8

ID ADJ58694 standard; protein; 468 AA.

XX ADJ58694;

DT 06-MAY-2004 (first entry)

DE Rat rectal protein.

KW Tissue growth; rect. protein; organ failure; foetal malformation;

KW tumour growth; renal tissue; cytostatic; vulnerary; nephroretropic; rat.

OS Rattus sp.

PN US6677135-B1.

PD 13-JAN-2004.

XX 06-NOV-1998; 98US-00187906.

Db 181 SMSNEVCNRRCKHCHALRQFFDKVPAKHSYGMFCSCRDIACTERRRQTIIVPCSYEBER 240
 QY 241 PNCISLSDSCCTNTYICSRRLADFFNQCOPESRSVNCLEKYNADCLAYSGLIGVTWTPN 300
 Db 241 PNCISLSDSCCTNTYICSRRLADFFNQCOPESRSVNCLEKYNADCLAYSGLIGVTWTPN 300
 QY 301 YVDSLSLVAPWCDCSNNGNDLEDCLKFNPKDNTCKNAIQAFNGSDVTMMQPAFV 360
 Db 301 YVDSLSLVAPWCDCSNNGNDLEDCLKFNPKDNTCKNAIQAFNGSDVTMMQPAFV 360
 QY 361 QTTATTTTAAFRVKNKPIGPAGSENEIPTHVLPICANTQAQTLKSNVSGSTHLCISDSDF 420
 Db 361 QTTATTTTAAFRVKNKPIGPAGSENEIPTHVLPICANTQAQTLKSNVSGSTHLCISDSDF 420
 QY 421 GKDGLAGASHITTKSMAPPCSCLSLPIVMTALALSYLAETS 468
 Db 421 GKDGLAGASHITTKSMAPPCSCLSLPIVMTALALSYLAETS 468

RESULT 10

AAW35333 standard; protein; 465 AA.

AC AAW35333;
 XX
 DT 01-MAY-1998 (first entry)

Human glial cell line-derived neurotrophic factor receptor.

DE Human glial cell line-derived neurotrophic factor; GDNF; receptor;
 KW treatment; dopaminergic nerve cell disorder; Parkinson's disease;
 KM Alzheimer's disease; amyotrophic lateral sclerosis; diabetes;
 KM Huntington's disease; glaucoma; retinal degeneration; hearing loss;
 KW gene therapy.

OS Homo sapiens.

XX MO9740152-A1.

XX 30-OCT-1997.

XX 15-APR-1997; 97WO-US006281.

XX 22-APR-1996; 96US-0015907P.

XX 09-MAY-1996; 96US-0017221P.

XX 14-APR-1997; 97US-00837199.

XX (AMGE-) AMGEN INC.

XX Fox GM, Wen D, Jing S;

XX WPI, 1997-535836/49.

XX N-PSDB; AAT88419.

XX Glial cell line derived neurotrophic factor receptor - useful to treat

XX dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's

XX disease.

XX Claim 1; Page 91-93; 196pp; English.

XX The present sequence is the human glial cell line-derived neurotrophic
 CC factor (GDNF) receptor, which can be used to treat dopaminergic nerve
 CC cell disorders, e.g. Parkinson's and Alzheimer's disease or amyotrophic
 CC lateral sclerosis, complications of diabetes and Huntington's disease and
 CC (optionally in combination with GDNF) glaucoma, retinal degeneration and
 CC hearing loss caused by injury to inner ear sensory neurons. The receptor
 CC can also be used to block unwanted GDNF activity, analyse GDNF related
 CC molecules and stabilise GDNF in pharmaceutical formulations. Receptor
 CC expressing cells, preferably transfected ex vivo, can be used similarly
 CC by implantation, and the use of the receptor cDNA in gene therapy is also
 CC contemplated. Probes based on the cDNA can be used to identify GDNF
 CC responsive cells and tissues, e.g. to identify patients who would benefit

CC from GDNF therapy, and abnormalities in receptor expression, and to
 CC isolate molecules that form a complex with the cDNA or are
 CC homologous/cross-reactive with the cDNA. Anti-receptor antibodies.
 CC oligonucleotides derived from the cDNA and animal models that overexpress
 CC the receptor can be used to study the biological function of GDNF.
 CC knockout transgenic animals can be used to detect GDNF dependent neurons
 CC or processes and the antibody can be used to detect GDNF dependent neurons
 CC receptor. The receptor binds GDNF specifically and with high affinity,
 CC acting as part of a complex that mediates/enhances signal transduction by
 CC GDNF, i.e. increasing dopamine uptake in dopaminergic cells

XX Sequence 465 AA;

Query Match 93.1%; Score 2316.5; DB 2; Length 465;
 Best Local Similarity 92.7%; Pred. No. 9.6e-185;
 Matches 434; Conservative 18; Mismatches 13; Indels 3; Gaps 2;

QY 1 MFATLYPALPLDLMSABVSGDRLDCVNASDQCLEQSCSTKYRTLQCVAGKETNF 60
 Db 1 MFATLYPALPLDLMSABVSGDRLDCVNASDQCLEQSCSTKYRTLQCVAGKETNF 60
 QY 61 SLTSGLEAKDCRSAMEALKOKSLYNCRCKGKMKKNCIRIYWSWQSLQGNLDLSDP 120
 Db 61 SLTSGLEAKDCRSAMEALKOKSLYNCRCKGKMKKNCIRIYWSWQSLQGNLDLSDP 120
 QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAKACNLDLDTCKYRSAYITPCTT 180
 Db 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAKACNLDLDTCKYRSAYITPCTT 180
 QY 181 SMSNEVCNRRCKHCHALRQFFDKVPAKHSYGMFCSCRDIACTERRRQTIIVPCSYEBER 240
 Db 181 SMSNEVCNRRCKHCHALRQFFDKVPAKHSYGMFCSCRDIACTERRRQTIIVPCSYEBER 240
 QY 241 PNCISLSDSCCTNTYICSRRLADFFNQCOPESRSVNCLEKYNADCLAYSGLIGVTWTPN 300
 Db 241 PNCISLSDSCCTNTYICSRRLADFFNQCOPESRSVNCLEKYNADCLAYSGLIGVTWTPN 300
 QY 301 YVDSLSLVAPWCDCSNNGNDLEDCLKFNPKDNTCKNAIQAFNGSDVTMMQPAFV 360
 Db 301 YVDSLSLVAPWCDCSNNGNDLEDCLKFNPKDNTCKNAIQAFNGSDVTMMQPAFV 360
 QY 361 QTTATTTTAAFRVKNKPIGPAGSENEIPTHVLPICANTQAQTLKSNVSGSTHLCISDSDF 420
 Db 361 QTTATTTTAAFRVKNKPIGPAGSENEIPTHVLPICANTQAQTLKSNVSGSTHLCISDSDF 420
 QY 421 GKDGLAGASHITTKSMAPPCSCLSLPIVMTALALSYLAETS 468
 Db 421 GKDGLAGASHITTKSMAPPCSCLSLPIVMTALALSYLAETS 468

RESULT 11

AAW84163 standard; protein; 465 AA.

XX AAW84163;

XX 25-MAR-1999 (first entry)

XX Glial cell-line derived neurotrophic factor receptor-alpha cDNA.

XX Human; glial cell-line derived neurotrophic factor receptor-alpha;

XX GDNF-alpha; glial cell line-derived neurotrophic factor; GDNF;

XX neurotun; signal transduction; dopaminergic nerve cell;

XX Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;

XX neurological disorder; diabetes; glaucoma; sensory neuron;

XX retinal ganglion cell degeneration; sensory neuropathy; retinopathy;

XX gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..18

XX /note="putative signal peptide"

RESULT 14
ADD46325 standard; protein; 465 AA.
AC ADD46325;
DT 29-JAN-2004 (first entry)
XX Human Protein P56159, SEQ ID NO 12000.
DE
XX
XX Human; pain; neuronal tissue; gene therapy;
KM spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.
OS Homo sapiens.
XX WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GEHO) GEN HOSPITAL CORP.
XX PA (FARB) BAYER AG.
XX PI Woolf C, D'ureo D, Befort K, Coetigan M;
XX DR WPI, 2003-268312/26.
XX DR GENBANK; P56159.
XX PT New composition comprising two or more isolated polypeptides, useful for
XX PT preparing a medicament for treating pain in an animal.
XX PS Claim 1, Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX therapy). The sequence presented is a human protein (shown in table 2 of
XX the specification) which is differentially expressed during pain. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from MRO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 465 AA;

Query Match 93.1%; Score 2316.5; DB 7; Length 465;
Best Local Similarity 92.7%; Pred. No. 9, 6e-185;
Matches 434; Conservative 18; Mismatches 13; Indels 3; Gaps 2;

QY 1 MFATLYPALPLDILMSAEVSGGDRLCDVKASDQCLKEQSCSTKRTTLRQCVAKKETNF 60
DB 1 MFATLYPALPLDILMSAEVSGGDRLCDVKASDQCLKEQSCSTKRTTLRQCVAKKETNF 60
QY 61 SLTSGLEARDCEKSAEALKQSLVNCRCRCKGKKEKNCRLRYWMSYQSLQGNLDLSDP 120
DB 61 SLTSGLEARDCEKSAEALKQSLVNCRCRCKGKKEKNCRLRYWMSYQSLQGNLDLSDP 120
QY 121 YEPVNSRLDIFRAVPFISDVEFQVVEHISKGNCCDAACANLDDPCCKYRSAYITPCTT 180
DB 121 YEPVNSRLDIFRAVPFISDVEFQVVEHISKGNCCDAACANLDDPCCKYRSAYITPCTT 180
QY 181 SMSNEVCNRRCKKALRQFPDKVPAGSYGMFLFCSCRDIACTERRRQTTVPVCSYEBER 240
DB 181 SVSNDVCNRRCKKALRQFPDKVPAGSYGMFLFCSCRDIACTERRRQTTVPVCSYEBER 240
QY 241 PNCLSLQDSCKTNYICRSRLADFTNCOPESSVSCLKENYADCLLAISGLIGTWTPN 300
DB 241 PNCLSLQDSCKTNYICRSRLADFTNCOPESSVSCLKENYADCLLAISGLIGTWTPN 300
QY 301 YVDSSLSVAPWCDCNSGNDLEDCLKFLNFKDNTCLKNALQAFGNGSDVTWMOAPAPV 360
DB 301 YVDSSLSVAPWCDCNSGNDLEDCLKFLNFKDNTCLKNALQAFGNGSDVTWMOAPAPV 360
QY 361 QTTATTTTAFRVKNKPLCPAGSENEIPHYVLPCCANLQAKLKSVNSGTHLCLSDSD 420
DB 361 QTTATTTTAFRVKNKPLCPAGSENEIPHYVLPCCANLQAKLKSVNSGTHLCLSDSD 420
QY 421 GRDGLAGASHITTKSMAPSCSLSLPVMLTAAALLSYLAETS 468
DB 421 EKEGL-GASSHITTKSMAPSCSLSLPVLVLTALSTLL--SLTETS 465

RESULT 15
ADE60802 standard; protein; 465 AA.
ID ADE60802
XX
XX ADE60802;
XX
XX 29-JAN-2004 (first entry)
XX
XX Human Protein P56159, SEQ ID NO 6714.
XX
XX Human; pain; neuronal tissue; gene therapy;
XX KM spinal segmental nerve injury; chronic constriction injury; CCI;
XX KM spared nerve injury; SNI; Chung.
XX
XX Homo sapiens.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX PF 14-AUG-2002; 2002WO-US025765.
XX
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX
XX PA (GEHO) GEN HOSPITAL CORP.
XX PA (FARB) BAYER AG.
XX
XX Woolf C, D'ureo D, Befort K, Coetigan M;
XX DR WPI, 2003-268312/26.
XX DR GENBANK; P56159.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1, Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated RNA or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNII) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at [ftp.wipo.int/pub/publ/published_poc_sequences](http://wipo.int/pub/publ/published_poc_sequences).

SQ Sequence 465 AA;

Query Match 93.1%; Score 2316.5; DB 7; Length 465;

Matches 434; Conservative 18; Mismatches 13;

Matches 434; Conservative 18; Mismatches 13; Indels 3; Gaps 2

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Dd	1	MFATLTYFALPLLLDLMSAEVSGSDRLDCKYASDOCLKEOSCSKRTTLEOCVAKKETNF	60
Qy	61	SLTSGLEANDCECRSAMEALKOKSLYNCRCKRGKKEKNCRLIYMSYQSLQNDLLEDS	120
Dd	61	SLASGLEANDCECRSAMEALKOKSLYNCRCKRGKKEKNCRLIYMSYQSLQNDLLEDS	120
Qy	121	YEPVNSRLSDIRRAVFISDVFPQOVEHISKGNCCCLDAAKCANLDDTCCKTRSAVITTECTT	180
Dd	121	YEPVNSRLSDIRRAVFISDVFPQOVEHIIPIKGNCCCLDAAKCANLDDTCCKTRSAVITTECTT	180
Qy	181	SMSNEVCNRRKCHKALROFFDKYPAKHSYMTLFCSCRDIACTERBRQTIYPVCSYEERER	240
Dd	181	SYSNDVCNRRKCHKALROFFDKYPAKHSYMTLFCSCRDIACTERBRQTIYPVCSYEERER	240
Qy	241	PNCGLSDSCKTNYYICRSRLADFTNCCQPESSRVSNCLENYADCLLAYSGLIGTWTPTN	300
Dd	241	PNCMLNODSCKTNYYICRSRLADFTNCCQPESSRVSNCLENYADCLLAYSGLIGTWTPTN	300
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Dd	301	YVDSSSLISVAPMCDGCSGNDLEDCLEKLFNFPDONTCLKNAIQAFGSGSDVYTMQAPAPV	360
Qy	361	QTTTATTTTAFRVKNRPLGPAGSENEIPTHVLPCCANIQAKLKSNSVGSHTLCLTSDSF	420
Dd	361	QTTTATTTTALRVKNRPLGPAGSENEIPTHVLPCCANIQAKLKSNSVGSHTLCLTSGNY	420
Qy	421	GDDGLAGASHITTKSMAAPSCSLSGLPLMTLTAALLSVSLAETS	468
Dd	421	EKEGL-GASSHITTKSMAAPSCSLSGLPLLVLTALSTLL--SLTETS	465

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 17, 2005, 08:52:18 ; Search time 139 Seconds
(Without alignments)
1101.790 Million cell updates/sec

Title: US-10-033-350-2
Perfect score: 2488
Sequence: 1 MEALATYFALPLDILMSAE.....PVLMTALMALSVLSAERS 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1380268 segs, 327241040 residues
Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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20: /cgn2_6/prodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2488	100.0	468	14	US-10-033-350-2
2	2488	100.0	468	14	US-10-357-822-21
3	2488	100.0	468	14	US-10-155-693-4
4	2488	100.0	468	14	US-10-673-007-1
5	2316.5	93.1	465	14	US-10-357-822-22
6	2316.5	93.1	465	14	US-10-155-693-2
7	2316.5	93.1	465	14	US-10-295-027-84
8	2316.5	93.1	465	14	US-10-058-270A-24
9	2311.5	92.9	463	14	US-10-155-693-12
10	2310.5	92.9	465	16	US-10-673-007-8
11	2309.5	92.8	465	14	US-10-155-693-6
12	2306.5	92.7	463	14	US-10-155-693-10
13	2278	91.6	460	14	US-10-241-220-62

14	1431.5	57.5	294	14	US-10-155-693-16	Sequence 16, Appl
15	1220	49.0	232	14	US-10-155-693-14	Sequence 14, Appl
16	1120.5	45.0	464	14	US-09-388-316-6	Sequence 6, Appl1
17	1120.5	45.0	464	14	US-10-357-822-6	Sequence 2, Appl1
18	1120.5	45.0	464	16	US-10-673-007-2	Sequence 3, Appl1
19	1117.5	44.9	464	14	US-09-388-316-3	Sequence 3, Appl1
20	1117.5	44.9	464	14	US-10-357-822-3	Sequence 3, Appl1
21	1108.5	44.6	464	16	US-10-673-007-9	Sequence 18, Appl
22	1100	44.2	664	9	US-09-388-316-18	Sequence 18, Appl
23	1100	44.2	664	14	US-10-357-822-18	Sequence 16, Appl
24	1099.5	44.2	664	14	US-09-388-316-16	Sequence 16, Appl
25	1099.5	44.2	664	14	US-10-357-822-16	Sequence 16, Appl
26	1098.5	44.2	445	16	US-10-673-007-11	Sequence 11, Appl
27	1035.5	41.6	219	14	US-10-155-693-18	Sequence 18, Appl
28	983.5	39.5	209	14	US-10-155-693-20	Sequence 20, Appl
29	946.5	26.0	147	14	US-10-155-693-22	Sequence 22, Appl
30	617.5	24.8	141	14	US-10-155-693-24	Sequence 24, Appl
31	573	23.0	120	9	US-09-864-761-47340	Sequence 47340, A
32	511	20.5	400	9	US-09-820-920-63	Sequence 63, Appl
33	511	20.5	400	9	US-09-828-366-16	Sequence 16, Appl
34	505.5	20.3	397	9	US-09-820-920-64	Sequence 64, Appl
35	227	9.1	132	10	US-09-866-050A-709	Sequence 709, App
36	214	8.6	394	15	US-10-369-904-2	Sequence 2, Appl1
37	148	5.9	3051	15	US-10-369-493-5866	Sequence 5866, Ap
38	136	5.5	207	9	US-09-893-737-160	Sequence 160, App
39	131	5.3	2471	15	US-10-190-115-27	Sequence 27, Appl
40	131	5.3	2471	15	US-10-369-072-27	Sequence 27, Appl
41	129	5.2	770	14	US-10-281-478-11	Sequence 11, Appl
42	123.5	5.0	2195	15	US-10-369-493-6828	Sequence 6828, Ap
43	122	4.9	2503	16	US-10-322-281-723	Sequence 723, App
44	121.5	4.9	886	9	US-09-992-647-11	Sequence 11, Appl
45	121.5	4.9	886	14	US-10-225-567A-50	Sequence 90, Appl

ALIGNMENTS

RESULT 1
US-10-033-350-2
; Sequence 2, Application US/10033350
; Publication No. US2003002284A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
Klein, Robert D.
Moore, Mark W.
Rosenthal, Arnon
Ryan, Anne M.
TITLE OF INVENTION: USES OF GDNF AND GDNF RECEPTOR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/033,350
FILING DATE: 02-Mar-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/860,370
FILING DATE: <Unknown>
APPLICATION NUMBER: PCT/US97/04363
FILING DATE: 13-Mar-1997
APPLICATION NUMBER: 08/615902
FILING DATE: 14-MAR-1996
APPLICATION NUMBER: 08/618236

	FILING DATE: 14-MAR-1996
	ATTORNEY/AGENT INFORMATION:
	NAME: torchia, PhD., timothy E.
	REGISTRATION NUMBER: 36,700
	REFERENCE/DOCKET NUMBER: P0996P1PCT
	TELECOMMUNICATION INFORMATION:
	TELEPHONE: 650/225-8674
	TELEFAX: 650/952-9881
	INFORMATION FOR SEQ ID NO: 2:
	SEQUENCE CHARACTERISTICS:
	LENGTH: 468 amino acids
	TYPY: Amino Acid
	TOPOLOGY: Linear
	FEATURE:
	NAME/KEY: Extracellular Domain
	LOCATION: 25
	IDENTIFICATION METHOD:
	OTHER INFORMATION:
	FEATURE:
	NAME/KEY: Mature Protein N-terminal
	LOCATION: 25-427
	IDENTIFICATION METHOD:
	OTHER INFORMATION:
	FEATURE:
	NAME/KEY: Potential Glycosylation Site
	LOCATION: 349
	IDENTIFICATION METHOD:
	OTHER INFORMATION:
	FEATURE:
	NAME/KEY: Potential Glycosylation Site
	LOCATION: 408
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	OTHER INFORMATION:
	FEATURE:
	NAME/KEY: Potential Glycosylation Site
	LOCATION: 61
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	US-10-033-350-2
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	Best Local Similarity 100.0%; Pred. No. 7,8e-210;
	Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
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; Sequence 21, Application US/10357822
; Publication No. US20030110525A1
; GENERAL INFORMATION:
; APPLICANT: KLEIN, ROBERT D.
; APPLICANT: ROSENTHAL, ARNON
; APPLICANT: HYNES, MARY A.
; TITLE OF INVENTION: NEOTURIN RECEPTOR
; FILE REFERENCE: GENENT.45A2DVA
; CURRENT APPLICATION NUMBER: US/10/357,822
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/388,316C
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: 09/024,665
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: 60/063,258
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/049,818
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: 60/038,839
; PRIOR FILING DATE: 1997-02-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-357-822-21

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Qy	61	SLTSGLEADECBSAMEALKOKSLYNCRCKRGMKEKNCIRIYWSYOSIQNDLLEDSP	120	
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Db	121	YEYVNSRLSDIRAPAFISDVFOQVEHISKNNCLDAAKCNLDPTCKKYRSAYITPCTT	180	
Qy	181	SMSNEVCNRKCKHAKLRQFEDKVPKASGYMLFPCSCRDIACTERRRQTIYVPCSYEERER	240	
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Db	241	PNCLSLQDSCKTNYICRSHLADFFNQCPEBSRSISNCLKENYADCLLAYSGLIGYMPFN	300	
Qy	301	YVDSSSLSYAAPWCDCSNGNDLEDCLKLFNFKONTCLKAIAQAFNGSGDVTYMQPAPFV	360	
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US-10-155-693-4
; Sequence 4, Application US/10155693
; Publication No. US20030175876A1
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUOJIAN
; APPLICANT: MEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/10/155,693
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US/08/837,199
; PRIOR FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 468
; TYPE: PRT
; ORGANISM: RAT
US-10-155-693-4

Query Match      100.0%; Score 2488; DB 14; Length 468;
Best Local Similarity 100.0%; Pred. No. 7,8e-210;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MFATATYFALPLDLMSAEVSGDRLDCKYASDQCKEOSTKRYTRLQCVAGKETNF 60
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DB 61 SLTSGLEADDECSAMEALQKSLYNCRCKRGKKEKNCIRIYMSYQSLQGNLDLSDP 120
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DB 121 YEPVNSRLSDIFRAVPEISDVFOVEHISKGNCLDAKACNLDPTCKKRSAYITPCTT 180
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DB 181 SMSNEVCNRRKCKHAKLROFPDKVPAGHSYGMFCSCRDIACTERRRQTIIVPVCSYERER 240
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QY 361 QTTTATTTTAFRYKRNKPLPAGSENEIPTHVLPCCANLQAKKSNVSGSTHCLSDSDP 420
DB 361 QTTTATTTTAFRYKRNKPLPAGSENEIPTHVLPCCANLQAKKSNVSGSTHCLSDSDP 420
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RESULT 4
US-10-673-007-1
; Sequence 1, Application US/10673007
; Publication No. US20040126819A1
; GENERAL INFORMATION:
; APPLICANT: Ibanez, Carlos F.
; APPLICANT: Artumae, Urmaz
; APPLICANT: Sarioja, Hannu
; APPLICANT: Suanto, Pietro
; APPLICANT: Trupp, Miles
; APPLICANT: Saarna, Mart

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; TITLE OF INVENTION: Glial Cell Line-Derived Neurotropic Factor Receptors
; FILE REFERENCE: CEP0418
; CURRENT APPLICATION NUMBER: US/10/673,007
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/08/661,990
; PRIOR FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: 08/747,842
; PRIOR FILING DATE: 1996-11-13
; PRIOR APPLICATION NUMBER: 60/006,619
; PRIOR FILING DATE: 1995-11-13
; PRIOR APPLICATION NUMBER: 60/015,767
; PRIOR FILING DATE: 1996-04-16
; PRIOR APPLICATION NUMBER: 60/021,965
; PRIOR FILING DATE: 1996-06-27
; PRIOR APPLICATION NUMBER: 60/020,638
; PRIOR FILING DATE: 1996-06-27
; PRIOR APPLICATION NUMBER: 60/020,639
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-673-007-1

Query Match      100.0%; Score 2488; DB 16; Length 468;
Best Local Similarity 100.0%; Pred. No. 7,8e-210;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MFATATYFALPLDLMSAEVSGDRLDCKYASDQCKEOSTKRYTRLQCVAGKETNF 60
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DB 121 YEPVNSRLSDIFRAVPEISDVFOVEHISKGNCLDAKACNLDPTCKKRSAYITPCTT 180
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DB 181 SMSNEVCNRRKCKHAKLROFPDKVPAGHSYGMFCSCRDIACTERRRQTIIVPVCSYERER 240
QY 241 PNCLSLQDSCKTNYICRSRLADFTTNCOPESRSVSNCKENYADCLAYSGLIGTWTPN 300
DB 241 PNCLSLQDSCKTNYICRSRLADFTTNCOPESRSVSNCKENYADCLAYSGLIGTWTPN 300
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DB 301 YVDSSSLVAWPCDCSNGNDLEDCIKFLNPFKONTCLKNAIOAFNGSDVTWMOAPAPV 360
QY 361 QTTTATTTTAFRYKRNKPLPAGSENEIPTHVLPCCANLQAKKSNVSGSTHCLSDSDP 420
DB 361 QTTTATTTTAFRYKRNKPLPAGSENEIPTHVLPCCANLQAKKSNVSGSTHCLSDSDP 420
QY 421 GKDGLAGASHITTKSMAAPPSCSLSLPYMLTALALSVLSAETS 468
DB 421 GKDGLAGASHITTKSMAAPPSCSLSLPYMLTALALSVLSAETS 468

RESULT 5
US-10-357-822-22
; Sequence 22, Application US/10357822
; Publication No. US20030110525A1
; GENERAL INFORMATION:
; APPLICANT: KLEIN, ROBERT D.
; APPLICANT: ROSENTHAL, ARNON
; APPLICANT: HYNES, MARY A.
; TITLE OF INVENTION: NEURTURIN RECEPTOR
; FILE REFERENCE: GENENT, 45A2DV1

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CURRENT APPLICATION NUMBER: US/10/357,822
CURRENT FILING DATE: 2003-02-03
PRIORITY APPLICATION NUMBER: US/09/388,316C
PRIORITY FILING DATE: 1999-09-01
PRIORITY APPLICATION NUMBER: 09/024,665
PRIORITY FILING DATE: 1998-02-17
PRIORITY APPLICATION NUMBER: 60//063,258
PRIORITY FILING DATE: 1997-10-24
PRIORITY APPLICATION NUMBER: 60/049,818
PRIORITY FILING DATE: 1997-06-09
PRIORITY APPLICATION NUMBER: 60/038,839
PRIORITY FILING DATE: 1997-02-18
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 465
TYPE: PRT
ORGANISM: Homo sapiens
US-10-357-822-22

```

Query Match	Similarity	93.1%	Score 2316.5	DB 14	Length 465
Best Local	Similarity	92.7% <td>Pred. No. 9.1e-195</td> <td></td> <td></td>	Pred. No. 9.1e-195		
Matches 434	Conservative	18	Identities 13	Gaps 2	

Query	Db	Sequence	Score	Length	Identity	Gap
1	MFALTYALPLDLLMSAEVSGGRLLDVCVKSADOCLEKESQSTKRTLRQCAGKETNF	92.7%	2316.5	465	13	2
1	MFALTYALPLDLLMSAEVSGGRLLDVCVKSADOCLEKESQSTKRTLRQCAGKETNF	92.7%	2316.5	465	13	2
61	SLTSGLEAKDECRSAMEALKOKSLYNCRCKGMKKEKNCRLIYWSMYOSLGNDLLEDSP	92.7%	2316.5	465	13	2
61	SLTSGLEAKDECRSAMEALKOKSLYNCRCKGMKKEKNCRLIYWSMYOSLGNDLLEDSP	92.7%	2316.5	465	13	2
121	YEPVNSRLSDIFRAVPEFISDVFOQVEHTSKGNCCDPAACAKNLDPCKKYRSAYITPCTT	92.7%	2316.5	465	13	2
121	YEPVNSRLSDIFRAVPEFISDVFOQVEHTSKGNCCDPAACAKNLDPCKKYRSAYITPCTT	92.7%	2316.5	465	13	2
181	SMSNEVCNRRKCKHAKLROFPDVKYPAKHSYGMFCSCGRDIACERRRQTIIVPCSYBERER	92.7%	2316.5	465	13	2
181	SMSNEVCNRRKCKHAKLROFPDVKYPAKHSYGMFCSCGRDIACERRRQTIIVPCSYBERER	92.7%	2316.5	465	13	2
241	PNCISLQDSCKTNYICRSHLADPFNQCOPESBSVSNCKENYADCLLAYSGIIGVTMPN	92.7%	2316.5	465	13	2
241	PNCISLQDSCKTNYICRSHLADPFNQCOPESBSVSNCKENYADCLLAYSGIIGVTMPN	92.7%	2316.5	465	13	2
301	YVDSLSLVAAPDCDSNSGNDLEDCLKLFNFKDNTCLKNALQAFNGSDVMQMAPAV	92.7%	2316.5	465	13	2
301	YVDSLSLVAAPDCDSNSGNDLEDCLKLFNFKDNTCLKNALQAFNGSDVMQMAPAV	92.7%	2316.5	465	13	2
361	QTTATTTTAAFRKVKPKLPAGPAGSENEIPHYVPPCANLQAOGLKSNVSGSTHCLSDSDP	92.7%	2316.5	465	13	2
361	QTTATTTTAAFRKVKPKLPAGPAGSENEIPHYVPPCANLQAOGLKSNVSGSTHCLSDSDP	92.7%	2316.5	465	13	2
421	GKGLAGASSHTTYSMAAPPSCSLSSLEVTMLTALAALLSVSLAETS	92.7%	2316.5	465	13	2
421	GKGLAGASSHTTYSMAAPPSCSLSSLEVTMLTALAALLSVSLAETS	92.7%	2316.5	465	13	2

Query	Db	Sequence	Score	Length	Identity	Gap
1	MFALTYALPLDLLMSAEVSGGRLLDVCVKSADOCLEKESQSTKRTLRQCAGKETNF	92.7%	2316.5	465	13	2
1	MFALTYALPLDLLMSAEVSGGRLLDVCVKSADOCLEKESQSTKRTLRQCAGKETNF	92.7%	2316.5	465	13	2
61	SLTSGLEAKDECRSAMEALKOKSLYNCRCKGMKKEKNCRLIYWSMYOSLGNDLLEDSP	92.7%	2316.5	465	13	2
61	SLTSGLEAKDECRSAMEALKOKSLYNCRCKGMKKEKNCRLIYWSMYOSLGNDLLEDSP	92.7%	2316.5	465	13	2
121	YEPVNSRLSDIFRAVPEFISDVFOQVEHTSKGNCCDPAACAKNLDPCKKYRSAYITPCTT	92.7%	2316.5	465	13	2
121	YEPVNSRLSDIFRAVPEFISDVFOQVEHTSKGNCCDPAACAKNLDPCKKYRSAYITPCTT	92.7%	2316.5	465	13	2
181	SMSNEVCNRRKCKHAKLROFPDVKYPAKHSYGMFCSCGRDIACERRRQTIIVPCSYBERER	92.7%	2316.5	465	13	2
181	SMSNEVCNRRKCKHAKLROFPDVKYPAKHSYGMFCSCGRDIACERRRQTIIVPCSYBERER	92.7%	2316.5	465	13	2
241	PNCISLQDSCKTNYICRSHLADPFNQCOPESBSVSNCKENYADCLLAYSGIIGVTMPN	92.7%	2316.5	465	13	2
241	PNCISLQDSCKTNYICRSHLADPFNQCOPESBSVSNCKENYADCLLAYSGIIGVTMPN	92.7%	2316.5	465	13	2
301	YVDSLSLVAAPDCDSNSGNDLEDCLKLFNFKDNTCLKNALQAFNGSDVMQMAPAV	92.7%	2316.5	465	13	2
301	YVDSLSLVAAPDCDSNSGNDLEDCLKLFNFKDNTCLKNALQAFNGSDVMQMAPAV	92.7%	2316.5	465	13	2
361	QTTATTTTAAFRKVKPKLPAGPAGSENEIPHYVPPCANLQAOGLKSNVSGSTHCLSDSDP	92.7%	2316.5	465	13	2
361	QTTATTTTAAFRKVKPKLPAGPAGSENEIPHYVPPCANLQAOGLKSNVSGSTHCLSDSDP	92.7%	2316.5	465	13	2
421	GKGLAGASSHTTYSMAAPPSCSLSSLEVTMLTALAALLSVSLAETS	92.7%	2316.5	465	13	2
421	GKGLAGASSHTTYSMAAPPSCSLSSLEVTMLTALAALLSVSLAETS	92.7%	2316.5	465	13	2

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1      PRIOR APPLICATION NUMBER: US 60/011,221
2      PRIOR FILING DATE: 1996-05-09
3      NUMBER OF SEQ ID NOS: 47
4      SOFTWARE: PatentIn version 3.1
5      SEQ ID NO 2
6      LENGTH: 465
7      TYPE: PRT
8      ORGANISM: HUMAN
9      FEATURE:
10     NAME/KEY: misc_feature
11     LOCATION: (2078)..(2078)
12     OTHER INFORMATION: N in position 2078 indicates a position of divergence between dif
13     FEATURE:
14     NAME/KEY: misc_feature
15     LOCATION: (2107)..(2107)
16     OTHER INFORMATION: N in position 2107 indicates a position of divergence between dif
17     FEATURE:
18     NAME/KEY: misc_feature
19     LOCATION: (2241)..(2241)
20     OTHER INFORMATION: N in position 2241 indicates a position of divergence between dif
21     FEATURE:
22     NAME/KEY: misc_feature
23     LOCATION: (2250)..(2250)
24     OTHER INFORMATION: N in position 2250 indicates a position of divergence between dif
25     FEATURE:
26     NAME/KEY: misc_feature
27     LOCATION: (2256)..(2294)
28     OTHER INFORMATION: N in positions 2256 to 2294 indicates positions of divergence be
29     OTHER INFORMATION: tween different receptor clones
30     US-10-155-693-2

```

Query Match	93.1%	Score 2316.5	DB 14	Length 465
Best Local Similarity	92.7%	Pred. No. 9.1e-195		
Matches 434	Conservative 18	Mismatches 13	Indels 3	Gaps 2
Qy	1	MFATLYFALPLDLLMSAEVSGGDRDLCVYASDQCLKEQSCSTKYRTLLRQVAKETNF	60	
Db	1	MFATLYFALPLDLLLSAEVSGGDRDLCVYASDQCLKEQSCSTKYRTLLRQVAKETNF	60	
Qy	61	SLTSGLEAKDECRGAMETLKKSLYNCRCKRMKKENKCRIRYWSYQSLQSGNDLLEDSP	120	
Db	61	SLASGLEAKDECRGAMETLKKSLYNCRCKRMKKENKCRIRYWSYQSLQSGNDLLEDSP	120	
Qy	121	YEPVNSRLSDI FRAVPEISDVFOQVEHI SKGNCCLDAAKCANLDDTCKYRSAYITPCTT	180	
Db	121	YEPVNSRLSDI FRAVPEISDVFOQVEHI SKGNCCLDAAKCANLDDTCKYRSAYITPCTT	180	
Qy	181	SMSNEVCNRKCHALAKQFPDKVPAAKHSYGMLEFSCGDIACTEBRROTIVPVCSYEER	240	
Db	181	SMSNEVCNRKCHALAKQFPDKVPAAKHSYGMLEFSCGDIACTEBRROTIVPVCSYEER	240	
Qy	241	PNCISLDQSCKTYNICRSLADPEFTNCPESRSVSNCLKENYADCLLAYSGLIGYWTNP	300	
Db	241	PNCISLDQSCKTYNICRSLADPEFTNCPESRSVSNCLKENYADCLLAYSGLIGYWTNP	300	
Qy	301	YVDSSSLSVAPMCCCSNSGNDLEDCLEFLNPFNDNTCLKNAIQAFNGSGVYTMWQAPPV	360	
Db	301	YVDSSSLSVAPMCCCSNSGNDLEDCLEFLNPFNDNTCLKNAIQAFNGSGVYTMWQAPPV	360	
Qy	361	QTTATATTTAFRVNKRKLGPAGSENEIPTVLEPPCANLQAKLKSUNVSGTHLCLSDSP	420	
Db	361	QTTATATTTAFRVNKRKLGPAGSENEIPTVLEPPCANLQAKLKSUNVSGTHLCLSDSP	420	
Qy	421	GKQGLAGASHITTKSMAAPPSCGSLSPVLMLTALAAILSVLAETS	468	
Db	421	EKEQPLGASSHITTKSMAAPPSCGSLSPVLMLTALAAILSVLAETS	465	

RESULT 7

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US-10-295-027-84
? Sequence 84, Application US/10295027
? Publication No. US20030232350A1
? GENERAL INFORMATION:
? APPLICANT: Afar, Daniel
? APPLICANT: Aziz, Natasha
? APPLICANT: Ginsberg, Wendy M.
? APPLICANT: Gish, Kurt C.
? APPLICANT: Glynn, Richard
? APPLICANT: Heyez, Peter A.
? APPLICANT: Mack, David H.
? APPLICANT: Murray, Richard
? APPLICANT: Watson, Susan R.
? APPLICANT: Eos Biotechnology, Inc.
? TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
? FILE REFERENCE: 018501-012500US
? CURRENT APPLICATION NUMBER: US/10/295,027
? CURRENT FILING DATE: 2002-11-13
? PRIOR APPLICATION NUMBER: US 09/663,733
? PRIOR FILING DATE: 2000-09-15
? PRIOR APPLICATION NUMBER: US 60/350,666
? PRIOR FILING DATE: 2001-11-13
? PRIOR APPLICATION NUMBER: US 60/335,394
? PRIOR FILING DATE: 2001-11-15
? PRIOR APPLICATION NUMBER: US 60/332,464
? PRIOR FILING DATE: 2001-11-21
? PRIOR APPLICATION NUMBER: US 60/334,393
? PRIOR FILING DATE: 2001-11-29
? PRIOR APPLICATION NUMBER: US 60/340,376
? PRIOR FILING DATE: 2001-12-14
? PRIOR APPLICATION NUMBER: US 60/347,211
? PRIOR FILING DATE: 2002-01-08
? PRIOR APPLICATION NUMBER: US 60/347,349
? PRIOR FILING DATE: 2002-01-10
? PRIOR APPLICATION NUMBER: US 60/355,250
? PRIOR FILING DATE: 2002-02-08
? PRIOR APPLICATION NUMBER: US 60/356,714
? PRIOR FILING DATE: 2002-02-13
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 1386
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 84
? LENGTH: 465
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-10-295-027-84

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[illegible]

Db 301 YIDSSLSVAAPMCDSCNSGNDLBECKTFNFKDXTCKKMAIQAFONGSDVTVWQAPFV 360

QY 361 OTTATTTTAAKVKKPLGPAGSENEIPTHVLPCCANIQAOKLKSNSGSTHLCSDSP 420

Db 361 OTTATTTTAAKVKKPLGPAGSENEIPTHVLPCCANIQAOKLKSNSGNTHLCISNGY 420

QY 421 GKDGAGASSHITTKSMAAPSCSLSLPVLMILTALALSVSLAETS 468

Db 421 EKEGL-GASSHITTKSMAAPSCGSLPLVLVVTALSTLL--SLRETS 465

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RESULT 8
US-10-058-270A-24
; Sequence 24, Application US/10058270A
; Publication No. US20040029114A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Afar, Daniel
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Breast Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Breast Cancer
; FILE REFERENCE: 018501-005210US
; CURRENT APPLICATION NUMBER: US/10/058, 270A
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 60/263,965
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/265,928
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/829,472
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 60/282,698
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 60/288,590
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,443
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-058-270A-24

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Query Match	Similarity	93.1%	Score	2316.5	DB 15	Length	465
Best Local	Similarity	92.7%	Pred. No.	9.1e-195			
Matches	434	Conservative	18	Mismatches	13	Indels	3
						Gaps	2
QY	1	MFATLYPALPLDLLMSAEVSGGDRDL	CVKASDQCLKEQSCSTYRILROC	VAGKETNF	60		
DB	1	MFATLYPALPLDLLLSAEVSGGDRDL	CVKASDQCLKEQSCSTYRILROC	VAGKETNF	60		
QY	61	SLTSLLEAKDECRSMEALKQSL	YNCRCKRKMKKEKQCLRI	YMSYOSLQGNLLEDSP	120		
DB	61	SLASLEAKDECRSMEALKQSL	YNCRCKRKMKKEKQCLRI	YMSYOSLQGNLLEDSP	120		
QY	121	YEPVNSRLSDI	PRAPFLISDVAFQVQVEH	SKGNNCILDAKACMLDPTCKKYRSAYITPCTT	180		
DB	121	YEPVNSRLSDI	FRVVPFLISDVAFQVQVEH	PKGNNCILDAKACMLDPTCKKYRSAYITPCTT	180		
QY	181	SMSNEVCNRKRCKHAKLQF	FDKVPKHSYGMFLFCSCRDIACTERRRQTI	VPVCSYEERER	240		
DB	181	SVSNDVCCRKRCKHAKLQF	FDKVPKHSYGMFLFCSCRDIACTERRRQTI	VPVCSYEERER	240		
QY	241	PNCISLADQCKNTNYICRSRLAD	FFTNCPESHRSVSNCLKENYADCL	LAYSGLIGVTPTN	300		
DB	241	PNCISLADQCKNTNYICRSRLAD	FFTNCPESHRSVSNCLKENYADCL	LAYSGLIGVTPTN	300		
QY	301	YVDSSSLVAAPWCDCSNGSND	LEDCLKLPLNFKNQNTCL	KNALQAFNGSGDVTMMQAPFV	360		
DB	301	YIDSSSLVAAPWCDCSNGSND	LEDCLKLPLNFKNQNTCL	KNALQAFNGSGDVTMMQAPFV	360		

QY 361 OTTATTTTAAVRVKKPLGPAGSENEIPTHVLPCCANLQAQKLKSNVSGSTHLCISDSDF 420
Db 361 OTTATTTTAAVRVKKPLGPAGSENEIPTHVLPCCANLQAQKLKSNVSGSTHLCISNGNY 420
QY 421 GKDGAGASSHITTKSMAAPBSCGSLSPVMTLTAALLSVLAETS 468
Db 421 EKEGL-GASSHITTKSMAAPBSCGSLSPVMTLTAALLSVLAETS 465

RESULT 9

US-10-155-693-12
; Sequence 12, Application US/10155693
; Publication No. US20030175876A1
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUOJIAN
; APPLICANT: WEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/10/155,693
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US/08/837,199
; PRIOR FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 463
; TYPE: PRT
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(539)
; OTHER INFORMATION: No. US20030175876A1= "1 to 539 18 -237 to 301 of Figure 5 21bcon
; US-10-155-693-12

Query Match 92.9%; Score 2311.5; DB 14; Length 463;
Best Local Similarity 92.9%; Pred. No. 2.5e-194;
Matches 430; Conservative 20; Mismatches 12; Indels 1; Gaps 1;
QY 1 MFATLTYALPLDILMSAEVSGGRLDVCVKSDDCKECSSTKYRTLROCVAGKETNF 60
Db 1 MFATLTYALPLDILMSAEVSGGRLDVCVKSDDCKECSSTKYRTLROCVAGKETNF 60
QY 61 SLTSGLEAKDECRSAMEALKOKSLYNCRCKRMKKEKNCRLIYWSMYOSLGNDLLEDSF 120
Db 61 SLTSGLEAKDECRSAMEALKOKSLYNCRCKRMKKEKNCRLIYWSMYOSLGNDLLEDSF 120
QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAKACNLDCTCKYRSAYITPCTT 180
Db 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAKACNLDCTCKYRSAYITPCTT 180
QY 181 SMSNEVCNRKCHKALROFPDVKVPAKHSYGMLFCSCRDIACCTERRRQTIIVPCSYEERER 240
Db 181 SVSNDVCNRKCHKALROFPDVKVPAKHSYGMLFCSCRDIACCTERRRQTIIVPCSYEERER 240
QY 241 PNCNLSDSCSKTNYICRSRLADFTNCPESRSVSNCKENYADCLLAYSGLIGVTMPN 300
Db 241 PNCNLSDSCSKTNYICRSRLADFTNCPESRSVSNCKENYADCLLAYSGLIGVTMPN 300
QY 301 YVDSLSVAAPWCDCSNGNDLEBCKLNFKNKNTCLKNAIQAFGNSDVTWQPAFPV 360
Db 301 YVDSLSVAAPWCDCSNGNDLEBCKLNFKNKNTCLKNAIQAFGNSDVTWQPAFPV 360
QY 361 OTTATTTTAAVRVKKPLGPAGSENEIPTHVLPCCANLQAQKLKSNVSGSTHLCISDSDF 420
Db 361 OTTATTTTAAVRVKKPLGPAGSENEIPTHVLPCCANLQAQKLKSNVSGSTHLCISNGNY 420
QY 421 GKDGAGASSHITTKSMAAPBSCGSLSPVMTLTAALLSVLAETS 463

Db 421 EKEGL-GASSHITTKSMAAPBSCGSLSPVMTLTAALLSVLAETS 462

RESULT 10

US-10-673-007-8
; Sequence 8, Application US/10673007
; Publication No. US20040126819A1
; GENERAL INFORMATION:
; APPLICANT: Ibanez, Carlos F.
; APPLICANT: Arumae, Urmas
; APPLICANT: Saviola, Hannu
; APPLICANT: Suvanto, Petri
; APPLICANT: Trupp, Miles
; APPLICANT: Saarna, Mart
; TITLE OF INVENTION: Glial Cell Line-Derived Neurotrophic Factor Receptors
; FILE REFERENCE: CEBH0418
; CURRENT APPLICATION NUMBER: US/10/673,007
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/08/861,990
; PRIOR FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: 08/747,842
; PRIOR FILING DATE: 1996-11-13
; PRIOR APPLICATION NUMBER: 60/006,619
; PRIOR FILING DATE: 1995-11-13
; PRIOR APPLICATION NUMBER: 60/015,767
; PRIOR FILING DATE: 1996-04-16
; PRIOR APPLICATION NUMBER: 60/021,965
; PRIOR FILING DATE: 1996-06-27
; PRIOR APPLICATION NUMBER: 60/020,638
; PRIOR FILING DATE: 1996-06-27
; PRIOR APPLICATION NUMBER: 60/020,639
; PRIOR FILING DATE: 1996-06-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-673-007-8

Query Match 92.9%; Score 2310.5; DB 16; Length 465;
Best Local Similarity 92.5%; Pred. No. 3.1e-194;
Matches 433; Conservative 18; Mismatches 14; Indels 3; Gaps 2;

QY 1 MFATLTYALPLDILMSAEVSGGRLDVCVKSDDCKECSSTKYRTLROCVAGKETNF 60
Db 1 MFATLTYALPLDILMSAEVSGGRLDVCVKSDDCKECSSTKYRTLROCVAGKETNF 60
QY 61 SLTSGLEAKDECRSAMEALKOKSLYNCRCKRMKKEKNCRLIYWSMYOSLGNDLLEDSF 120
Db 61 SLTSGLEAKDECRSAMEALKOKSLYNCRCKRMKKEKNCRLIYWSMYOSLGNDLLEDSF 120
QY 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAKACNLDCTCKYRSAYITPCTT 180
Db 121 YEPVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAKACNLDCTCKYRSAYITPCTT 180
QY 181 SMSNEVCNRKCHKALROFPDVKVPAKHSYGMLFCSCRDIACCTERRRQTIIVPCSYEERER 240
Db 181 SVSNDVCNRKCHKALROFPDVKVPAKHSYGMLFCSCRDIACCTERRRQTIIVPCSYEERER 240
QY 241 PNCNLSDSCSKTNYICRSRLADFTNCPESRSVSNCKENYADCLLAYSGLIGVTMPN 300
Db 241 PNCNLSDSCSKTNYICRSRLADFTNCPESRSVSNCKENYADCLLAYSGLIGVTMPN 300
QY 301 YVDSLSVAAPWCDCSNGNDLEBCKLNFKNKNTCLKNAIQAFGNSDVTWQPAFPV 360
Db 301 YVDSLSVAAPWCDCSNGNDLEBCKLNFKNKNTCLKNAIQAFGNSDVTWQPAFPV 360
QY 361 OTTATTTTAAVRVKKPLGPAGSENEIPTHVLPCCANLQAQKLKSNVSGSTHLCISDSDF 420
Db 361 OTTATTTTAAVRVKKPLGPAGSENEIPTHVLPCCANLQAQKLKSNVSGSTHLCISNGNY 420

QY 421 GKDLGASSHTTKSMAAPSCSLSLPYLMLTALAALISVLAETS 468
DB 421 EKEGL-GASSHTTKSMAAPSCSLSLPYLMLTALAALISVLAETS 465

RESULT 11

US-10-155-693-6
Sequence 6, Application US/10155693
Publication No. US20030175876A1
GENERAL INFORMATION:
APPLICANT: FOX, GARY M.
APPLICANT: JING, SHUOIAN
APPLICANT: MEN, DUANZHI
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
FILE REFERENCE: A-401C
CURRENT APPLICATION NUMBER: US/10/155,693
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US/08/837,199
PRIOR FILING DATE: 1997-04-14
PRIOR APPLICATION NUMBER: US 60/015,907
PRIOR FILING DATE: 1996-04-22
PRIOR APPLICATION NUMBER: US 60/017,221
PRIOR FILING DATE: 1996-05-09
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 465
TYPE: PRT
ORGANISM: HUMAN
FEATURE:
NAME/KEY: misc feature
LOCATION: (184)..(184)
OTHER INFORMATION: The 'Xaa' at location 184 stands for Lys, or Asn.
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(510)
OTHER INFORMATION: note="1 to 510 is -237 to 272 of Fig 5 Hsgr-21bf"
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(539)
OTHER INFORMATION: note="1 to 539 is -237 to 301 of Fig 5 Gdnfr"
FEATURE:
NAME/KEY: misc feature
LOCATION: (2078)..(2078)
OTHER INFORMATION: N in position 2078 indicates a position of divergence between dif
OTHER INFORMATION: ferent receptor clones
FEATURE:
NAME/KEY: misc feature
LOCATION: (2256)..(2294)
OTHER INFORMATION: N in positions 2256 to 2294 indicates positions of divergence bet
FEATURE:
NAME/KEY: misc feature
LOCATION: (1091)..(1091)
OTHER INFORMATION: N in position 1091 indicates any nucleic acid
US-10-155-693-6

Query Match 92.8%; Score 2309.5; DB 14; Length 465;
Best Local Similarity 92.5%; Pred. No. 3.7e-194;
Matches 433; Conservative 18; Mismatches 14; Indels 3; Gaps 2;

QY 1 MFLATLYFALPLDLILMSAEVSGDRLDCVKASDQCLKEQSCSTKYRTLRQCVAGKETNF 60
DB 1 MFLATLYFALPLDLILMSAEVSGDRLDCVKASDQCLKEQSCSTKYRTLRQCVAGKETNF 60
QY 61 SLTSGLEADECBSAMEALKQKSLYNCRCRKGKKEKNCRLRIYWSYQSLQGNLLEDSP 120
DB 61 SLTSGLEADECBSAMEALKQKSLYNCRCRKGKKEKNCRLRIYWSYQSLQGNLLEDSP 120
QY 121 YEFVNSRLSDIRPAVFISDVFOQVEHISKGNCLDAKACNLDPTCKYRSAYITPCTT 180
DB 121 YEFVNSRLSDIRPAVFISDVFOQVEHISKGNCLDAKACNLDPTCKYRSAYITPCTT 180

QY 181 SMSVENCRKCKHAROFEDKVPAGHYGMLFCSCORDIACERRROTIVPVCSYERER 240
DB 181 SVSKDVCCNRKCKHAROFEDKVPAGHYGMLFCSCORDIACERRROTIVPVCSYERER 240
QY 241 PNCISLQDSCKTYNYICRSRLADFTNCOPEBSRSVSNCLKENYADCLLAYSGLIGTWTPN 300
DB 241 PNCISLQDSCKTYNYICRSRLADFTNCOPEBSRSVSNCLKENYADCLLAYSGLIGTWTPN 300
QY 301 YDSSSLVAPWPCDCNSGNDLEDCIKFLNFKDNTCLNNAIOAFNGSDVTYMQAPAPV 360
DB 301 YDSSSLVAPWPCDCNSGNDLEDCIKFLNFKDNTCLNNAIOAFNGSDVTYMQAPAPV 360
QY 361 QTTATTTTAFRKNRPLDPAENSEIPTHVLPCCANLQAQKLSVSGTHCLDSDF 420
DB 361 QTTATTTTAFRKNRPLDPAENSEIPTHVLPCCANLQAQKLSVSGTHCLDSDF 420
QY 421 GKDLGASSHTTKSMAAPSCSLSLPYLMLTALAALISVLAETS 468
DB 421 EKEGL-GASSHTTKSMAAPSCSLSLPYLMLTALAALISVLAETS 465

RESULT 12

US-10-155-693-10
Sequence 10, Application US/10155693
Publication No. US20030175876A1
GENERAL INFORMATION:
APPLICANT: FOX, GARY M.
APPLICANT: JING, SHUOIAN
APPLICANT: MEN, DUANZHI
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
FILE REFERENCE: A-401C
CURRENT APPLICATION NUMBER: US/10/155,693
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US/08/837,199
PRIOR FILING DATE: 1997-04-14
PRIOR APPLICATION NUMBER: US 60/015,907
PRIOR FILING DATE: 1996-04-22
PRIOR APPLICATION NUMBER: US 60/017,221
PRIOR FILING DATE: 1996-05-09
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 463
TYPE: PRT
ORGANISM: HUMAN
FEATURE:
NAME/KEY: misc feature
LOCATION: (5)..(5)
OTHER INFORMATION: The 'Xaa' at location 5 stands for Thr, Ala, Pro, or Ser.
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(537)
OTHER INFORMATION: No. US20030175876A1e= "1 to 537 is -235 to 301 of Figure 5 21acon
FEATURE:
NAME/KEY: misc feature
LOCATION: (550)..(550)
OTHER INFORMATION: N in position 550 indicates any nucleic acid
US-10-155-693-10

Query Match 92.7%; Score 2306.5; DB 14; Length 463;
Best Local Similarity 92.7%; Pred. No. 6.8e-194;
Matches 429; Conservative 20; Mismatches 13; Indels 1; Gaps 1;

QY 1 MFLATLYFALPLDLILMSAEVSGDRLDCVKASDQCLKEQSCSTKYRTLRQCVAGKETNF 60
DB 1 MFLATLYFALPLDLILMSAEVSGDRLDCVKASDQCLKEQSCSTKYRTLRQCVAGKETNF 60
QY 61 SLTSGLEADECBSAMEALKQKSLYNCRCRKGKKEKNCRLRIYWSYQSLQGNLLEDSP 120
DB 61 SLTSGLEADECBSAMEALKQKSLYNCRCRKGKKEKNCRLRIYWSYQSLQGNLLEDSP 120
QY 121 YEFVNSRLSDIRPAVFISDVFOQVEHISKGNCLDAKACNLDPTCKYRSAYITPCTT 180
DB 121 YEFVNSRLSDIRPAVFISDVFOQVEHISKGNCLDAKACNLDPTCKYRSAYITPCTT 180


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Db      121 YEPVNSRLSDIFRVVPIISDVFOQVEH:PKGNNCIDAAKACNLDDICCKYRSAYITPCTT 180
Qy      181 SMSNEVCNRKCHALROFPDVKVPKSHYGM:FCSCRDIACTERRRQITVPCSYEBER 240
Db      181 SVSNDVCNRKCHALROFPDVKVPKSHYGM:FCSCRDIACTERRRQITVPCSYEBER 240
Qy      241 PNCISLSDSCXTNYICRSRLADFTNCPESRSVSNCKENYADCLAYSGIGVTMPN 300
Db      241 PNCISLSDSCXTNYICRSRLADFTNCPESRSVSNCKENYADCLAYSGIGVTMPN 300
Qy      301 YVDSSSLSVAVWCDCSNGNDLEDCLKFLNFKONTCLKNAIOAFNGSDVTVMQAPPV 360
Db      301 YVDSSSLSVAVWCDCSNGNDLEDCLKFLNFKONTCLKNAIOAFNGSDVTVMQAPPV 360
Qy      361 QTTATTTTAFRVKXKPLGPAGSENEIPTHVLPCCANLQAOXKSNVSGTHCLSDSD 420
Db      361 QTTATTTTAFRVKXKPLGPAGSENEIPTHVLPCCANLQAOXKSNVSGTHCLSDSD 420
Qy      421 GKDGAGASHITTKSMAAPSCSLSPVLMTLAALLSVA 463
Db      421 EKEGL-GASSHITTKSMAAPSCSLSPVLMTLAALLSVA 462

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RESULT 13
US-10-241-220-62
; Sequence 62, Application US/10241220
; Publication No. US20030148408A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P5010R1-US
; CURRENT FILING DATE: 2002-12-13
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 62
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-241-220-62

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Query Match      91.6%; Score 2278; DB 14; Length 460;
Best Local Similarity 91.7%; Pred. No. 2.2e-191;
Matches 429; Conservative 18; Mismatches 13; Indels 8; Gaps 3;

Qy      1 MFLATLTFALBLDLILMAEVSAGGRDLDCVAKSDOCLKEQSCSTYRTLRQCVAGKETNF 60
Db      1 MFLATLTFALBLDLILMAEVSAGGRDLDCVAKSDOCLKEQSCSTYRTLRQCVAGKETNF 60
Qy      61 SLTSGLEAKDCRSAMEALKOKSLVNCRCRGMKEKNCRLTYMGMYSLOQNDLLEBP 120
Db      61 SLTSGLEAKDCRSAMEALKOKSLVNCRCRGMKEKNCRLTYMGMYSLOQNDLLEBP 120
Qy      121 YEPVNSRLSDIFRVVPIISDVFOQVEH:SKGNCLDAKACNLDDICCKYRSAYITPCTT 180
Db      121 YEPVNSRLSDIFRVVPIISDVFOQVEH:SKGNCLDAKACNLDDICCKYRSAYITPCTT 180
Qy      181 SVSNDVCNRKCHALROFPDVKVPKSHYGM:FCSCRDIACTERRRQITVPCSYEBER 240
Db      181 SVSNDVCNRKCHALROFPDVKVPKSHYGM:FCSCRDIACTERRRQITVPCSYEBER 240
Qy      241 PNCISLSDSCXTNYICRSRLADFTNCPESRSVSNCKENYADCLAYSGIGVTMPN 300
Db      241 PNCISLSDSCXTNYICRSRLADFTNCPESRSVSNCKENYADCLAYSGIGVTMPN 300
Qy      301 YVDSSSLSVAVWCDCSNGNDLEDCLKFLNFKONTCLKNAIOAFNGSDVTVMQAPPV 360
Db      301 YVDSSSLSVAVWCDCSNGNDLEDCLKFLNFKONTCLKNAIOAFNGSDVTVMQAPPV 360

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Db      296 YVDSSSLSVAVWCDCSNGNDLEDCLKFLNFKONTCLKNAIOAFNGSDVTVMQAPPV 365
Qy      361 QTTATTTTAFRVKXKPLGPAGSENEIPTHVLPCCANLQAOXKSNVSGTHCLSDSD 420
Db      361 QTTATTTTAFRVKXKPLGPAGSENEIPTHVLPCCANLQAOXKSNVSGTHCLSDSD 420
Qy      421 GKDGAGASHITTKSMAAPSCSLSPVLMTLAALLSVA 468
Db      421 EKEGL-GASSHITTKSMAAPSCSLSPVLMTLAALLSVA 460

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RESULT 14
US-10-155-693-16
; Sequence 16, Application US/10155693
; Publication No. US20030175876A1
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUQIAN
; APPLICANT: WEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT FILING DATE: 2002-05-24
; CURRENT FILING DATE: 2002-05-24
; PRIOR FILING DATE: 1997-04-14
; PRIOR FILING DATE: 1996-05-09
; PRIOR FILING DATE: 1996-04-22
; PRIOR FILING DATE: 1996-04-22
; PRIOR FILING DATE: 1996-04-22
; PRIOR FILING DATE: 1996-04-22
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 294
; TYPE: PRT
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(2157)
; OTHER INFORMATION: No. US20030175876A1e "1 to 2157 is 814 to 2971 of Figure 5 29b'c"
; NAME/KEY: misc.feature
; LOCATION: (1204)-(1242)
; OTHER INFORMATION: N in positions 1204 to 1242 indicates positions of divergence bet
; OTHER INFORMATION: ween different receptor clones.
US-10-155-693-16

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Query Match      57.5%; Score 1431.5; DB 14; Length 294;
Best Local Similarity 89.9%; Pred. No. 2.9e-117;
Matches 267; Conservative 17; Mismatches 10; Indels 3; Gaps 2;

Qy      172 SAYITPCTTSMNVCNRKCHALROFPDVKVPKSHYGM:FCSCRDIACTERRRQITV 231
Db      1 SAYITPCTTSMNVCNRKCHALROFPDVKVPKSHYGM:FCSCRDIACTERRRQITV 231
Qy      232 VCSYERERPNCLSDSCXTNYICRSRLADFTNCPESRSVSNCKENYADCLAYSG 291
Db      232 VCSYERERPNCLSDSCXTNYICRSRLADFTNCPESRSVSNCKENYADCLAYSG 291
Qy      61 VCSYERERPNCLSDSCXTNYICRSRLADFTNCPESRSVSNCKENYADCLAYSG 120
Db      61 VCSYERERPNCLSDSCXTNYICRSRLADFTNCPESRSVSNCKENYADCLAYSG 120
Qy      121 LIGVTMPNYSVSSLSVAVWCDCSNGNDLEDCLKFLNFKONTCLKNAIOAFNGSDV 351
Db      121 LIGVTMPNYSVSSLSVAVWCDCSNGNDLEDCLKFLNFKONTCLKNAIOAFNGSDV 351
Qy      352 TMOQAPAVQTTATTTTAFRVKXKPLGPAGSENEIPTHVLPCCANLQAOXKSNVSGT 411
Db      352 TMOQAPAVQTTATTTTAFRVKXKPLGPAGSENEIPTHVLPCCANLQAOXKSNVSGT 411
Qy      412 HLCLSDSPFGKOGAGASHITTKSMAAPSCSLSPVLMTLAALLSVA 468
Db      412 HLCLSDSPFGKOGAGASHITTKSMAAPSCSLSPVLMTLAALLSVA 468
Qy      468 HLCLSDSPFGKOGAGASHITTKSMAAPSCSLSPVLMTLAALLSVA 468
Db      468 HLCLSDSPFGKOGAGASHITTKSMAAPSCSLSPVLMTLAALLSVA 468

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US-10-155-693-14
; Sequence 14, Application US/10155693
; Publication No. US20030175876A1
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUQIAN
; APPLICANT: WEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/10/155,693
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US/08/837,199
; PRIOR FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 232
; TYPE: PRT
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(699)
; OTHER INFORMATION: No. US20030175876A1e= "1 to 699 is 814 to 1512 of Figure 5 Hsgr-2
US-10-155-693-14

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Query Match          49.0%; Score 1220; DB 14; Length 232;
Best local Similarity 95.3%; Pred. No. 8,2e-99;
Matches 221; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY      172 SAYITPCTTSMNSNEVCNRKCKAKALRQFPDKVPKHSYGMWFCSCRDIACTERRRQTIYP 231
      1 SAYITPCTTSMNSNDVCNRKCKAKALRQFPDKVPKHSYGMWFCSCRDIACTERRRQTIYP 60

Db      232 VCSYERERENCISLQDSCCTNYICRSRLADFTNCPESRSVSNCKENYADCLAYSG 291
      61 VCSYERERENCISLQDSCCTNYICRSRLADFTNCPESRSVSNCKENYADCLAYSG 120

QY      292 LIGTVMTPNVVDSLSVAPWCCSNGNDLEDCLEKPLNFFKONTCLKNAIOAFNGSDV 351
      121 LIGTVMTPNVVDSLSVAPWCCSNGNDLEDCLEKPLNFFKONTCLKNAIOAFNGSDV 180

Db      352 TMMQAPAPVQTTTATTTAFRVKKNKPLGPAGSENEIPTHTVLPCCANLQAQKL 403
      181 TMMQAPAPVQTTTATTTAFRVKKNKPLGPAGSENEIPTHTVLPCCANLQAQKL 232

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Search completed: February 17, 2005, 09:48:37
 Job time : 143 secs

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